

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2003, 07:22:59 ; Search time 1244 Seconds
(without alignments)

13872.961 Million cell updates/sec

Title: US-10-020-338-8

Perfect score: 593
Sequence: 1 cccggtcgcaccagcgtccg.....catacaaatgtcacagc 593

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

tal number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Database :

GeneBml:*

1: gb_ba:*

2: gb_hcg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pac:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_srs:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_srs:*

28: em_un:*

29: em_vl:*

30: em_hcg_hum:*

31: em_hcg_inv:*

32: em_hcg_other:*

33: em_hcg_mus:*

34: em_hcg_pln:*

35: em_hcg_rtd:*

36: em_hcg_mam:*

37: em_hcg_vrt:*

38: em_sy:*

39: em_hcgo_hum:*

40: em_hcgo_mus:*

41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	332.8	56.1	1203	8	HVU249146
2	302.6	51.0	1062	8	AF035379
3	302.6	51.0	1250	8	AF112150
4	300.4	50.7	1345	6	AR042842
5	300.4	50.7	1345	6	AR095093
6	300.4	50.7	1345	6	AR113350
7	300.4	50.7	1345	6	AR200417
8	300.4	50.7	1345	8	MZEMASD
9	292.2	49.3	1186	8	SB032110
10	283.2	47.8	1285	8	AF058698
11	283.2	47.8	1289	6	BD012691
12	283.2	47.8	1289	8	AB003325
13	283.2	47.8	1289	23	BD005239
14	281.6	47.5	1347	8	AF345911
15	264.6	44.6	1161	8	AB007504
16	263	44.4	1124	8	AB041020
17	259.8	43.8	1101	8	AF139664
18	258.2	43.5	1196	8	HVU249144
19	258.2	43.5	1196	8	AF058697
20	252.4	42.6	1207	8	AF035378
21	201.2	33.4	809	8	AF198175
22	198.2	33.4	942	8	AB050657
23	195	32.9	1032	8	AF305696
24	195	32.9	1070	8	AF306349
25	188.6	31.8	974	8	OS0011675
26	188.6	31.8	1031	8	AF091158
27	186.8	31.5	1160	8	BPWADS3GN
28	184.4	31.1	1540	8	HVU249143
29	177.4	29.9	975	8	DC4271147
30	177.4	29.9	998	8	BPWADS4GN
31	175.8	29.6	1085	8	AF305076
32	173.6	29.3	966	8	BPWADS5GN
33	172.6	29.1	1055	8	MDJ759
34	168.2	28.4	1207	8	AF461740
35	166.8	28.1	914	8	AF139665
36	166.6	28.1	1140	8	PSA279089
37	166.6	28.1	1142	8	BOU67451
38	166.6	28.1	1230	8	MDU78948
39	165.8	28.0	909	8	AY040247
40	165.2	27.9	850	8	GHY9727
41	163.4	27.6	1054	6	AR063254
42	163.4	27.6	1054	6	ATAP1
43	163.4	27.6	1057	6	AR095090
44	163.4	27.6	1057	6	AR200414
45	163.4	27.6	1165	8	AY087956

ALIGNMENTS

RESULT 1
HVU249146
LOCUS HVU249146
DEFINITION Hordeum vulgare mRNA for MADS-box protein 8 (m8 gene).
ACCESSION AJ249146.1 GI:9367312
VERSION
KEYWORDS m8 gene; MADS-box protein 8.
SOURCE Hordeum vulgare subsp. vulgare.
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
REFERENCE
Schmitz, J., Franzen, R., Nguyen, T.H., Garcia-Maroto, F., Pozzi, C.,
1 (bases 1 to 1203)
Salamini, F. and Rohde, W., 1203 bp mRNA linear PLN 14-JUL-2000

TITLE Cloning, mapping and expression analysis of barley MADS-box genes
JOURNAL Plant Mol. Biol. 42 (6), 899-913 (2000)
MEDLINE 20346590
PUBMED 10890336
REFERENCE 2 (bases 1 to 1203)
AUTHORS Schmitz J.J.
TITLE Direct Submission
JOURNAL Submitted (20-AUG-1999) Schmitz J.J., Salamini, Max Planck Institut fuer Zuechtungsforchung, Carl von Linné Weg 10, 50829 Koeln, GERMANY

FEATURES
source Location/Qualifiers
1..1203
/organism="Hordeum vulgare subsp. vulgare"
/cultivar="Atlas"
/db_xref="taxon:112509"
/issue_type="Inflorance"
/clone_lib="lambda NM1149"
43..873
/gene="m8"
43..873
/gene="m8"
/codon_start=1
/product="MADS-box protein 8"
/protein_id="CB97354.1"
/db_xref="GI:9367313"
/translation="MGRGVOLKRIENKINROVTPSKRRNGLLKKAHEISVLCDAEVA
VVFSPKGLYEATDSMDKILERYERYSAEKALISAESSEGNMCHERYKIAKI
ETIOCKHLMEDDLSLNKEIQLEQLESLSKIRSKHLMESILOKERS
LOENKALKEIVEROKASROOQLQ0000Q00MEHQAVQVTHHTONQOAOQSS
SSSPFMRDOQAHPQONICSPYPTVMGEATATAAAPQOALRICLPWMLSHLNA"

BASE COUNT 356 a 288 c 308 g 251 t
ORIGIN

Query Match 56.1%; Score 332.8; DB 8; Length 1203;
Best Local Similarity 96.2%; Pred. No. 2,7e-69;
Matches 352; Conservative 0; Mismatches 12; Indels 2; Gaps 1;

228 CACAAAGCCGAGTAGATCGCGAATAGAGATATGGGTCCCGGGAAGTGCACCTGA 287
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10 CACAGAGCCGACACCTAGATCGTGAATCGGG-ATGGGTCCGGTAAGTGCACCTGA 67
|||
288 AGCGATAGAGACAAGATTAATCGCAGGTGACCTTCCCAAGCCCGCAAGGGCTCC 347
|||
68 AGCGATAGAGACAAGATTAATCGCAGGTGACCTTCCCAAGCCCGCAAGGGCTCC 127
|||
348 TGAAGAAGGCGACGAGATCTCGTCTGTGAAGGAGTGGCGGTGATGCTTCT 407
|||
128 TGAAGAAGGCGACGAGATCTCGTCTGTGAAGGAGTGGCGGTGATGCTTCT 187
|||
408 CCCCCAAGGCAAGCTTATGATAGCCCAAGATTCAGCATGCAAAATCTTGAAC 467
|||
188 CCCCCAAGGCAAGCTTATGATAGCCCAAGATTCAGCATGCAAAATCTTGAAC 247
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468 GTATAGAGCTACTCTTATGCTGAAGAGCTCTTATTCAGCTGATCGAAGTGAG 527
|||
248 GTTATAGAGCTACTCTTATGCTGAAGAGCTCTTATTCAGCTGATCGAAGTGAG 307
|||
528 GAAATTGTGCGACGAATACAGAACTTAAGCGGAAGATTGAGACCATCAAAAATGTC 587
|||
308 GGAATTGTGCGATGATACAGAACTTAAGCGGAAGATTGAGACCATCAAAAATGTC 367
|||
588 ACAAGC 593
|||
368 ACAAGC 373
|||

RESULT 2
AF035379 1062 bp mRNA linear PLN 29-JAN-1999
LOCUS Lolium temulentum MADS-box protein 2 (MADS2) mRNA, alternatively
DEFINITION spliced product, complete cds.
ACCESSION AF035379

VERSION AF035379.1 GI:4204233
KEYWORDS
SOURCE Lolium temulentum.
ORGANISM Lolium temulentum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Poace; Lolium.
1 (bases 1 to 1062)
Gocal.G.F.W., Blundell, C., Schwartz, O.M. and King, R.W.
Expression of Two APETALA1-Related Genes Changes During
Inflorescence Initiation of Lolium

REFERENCE
AUTHORS Unpublished
JOURNAL Unpublished
2 (bases 1 to 1062)
Gocal, G.F.W., King, R.W. and Blundell, C.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-1997) PBIO, Salk Institute, 10010 N. Torrey Pines
Rd., La Jolla, CA 92037, USA

FEATURES
source Location/Qualifiers
1..1062
/organism="Lolium temulentum"
/strain="Ceres"
/db_xref="taxon:34176"
1..1062
/gene="MADS2"
82..867
/gene="MADS2"
/note="AP1-related protein; alternatively spliced product"
/codon_start=1
/product="MADS-box protein 2"
/protein_id="AAD10626.1"
/db_xref="GI:4204234"
/translation="MGRGVOLKRIENKINROVTPSKRRNGLLKKAHEISVLCDAEVA
VVFSPKGLYEATDSMDKILERYERYSAEKALISAESSEGNMCHERYKIAKI
ETIOCKHLMEDDLSLNKEIQLEQLESLSKIRSKHLMESILOKERS
LOENKALKEIVEROKASROOQDQ00MROVTOQAQNPQAOQTSSSSPFMRDOQA
HAQOQICPVLVTMGGEAVAAAPGQGGQLRIGLCPWMLSHLNA"

BASE COUNT 316 a 254 c 288 g 204 t
ORIGIN

Query Match 51.0%; Score 302.6; DB 8; Length 1062;
Best Local Similarity 94.3%; Pred. No. 4.5e-62;
Matches 314; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

261 ATATGGGTGCGCGCAAGGTGACGTGAAGCGGATAGAGACAAGATTAATCGCAGGTGA 320
|||
80 AGATGGGTGCGCGCAAGGTGACGTGAAGCGGATAGAGACAAGATTAATCGCAGGTGA 139
|||
321 CCTTCTCAAGGCGCGCAAGGCTCTGGAAGAAGCGCAGAGATCTCGTCTGTG 380
|||
140 CATCTCCCAAGGCGCGCAAGGCTACTCAAGAAGCGCAGAGATCTCGTCTGTG 199
|||
381 AGCGGAGGTGCGCGCTCATGCTCTCTCCCAAGGCAAGGCTATGATAGTACGCGCAG 440
|||
200 AGCGGAGGTGCGCGCTCATGCTCTCTCCCAAGGCAAGGCTATGATAGTACGCGCAG 259
|||
441 ACTCCAGCATGGAACAATTTCTTGAACGTTATGAGCGCTACTTATGCTGAAGGCTC 500
|||
260 ACTCCAGCATGGAACAATTTCTTGAACGTTATGAGCGCTACTTATGCTGAAGGCTC 319
|||
501 TTAATTCAGCTGAATCTGAAGTGAAGGAAATTGTCGCAAGATACAGAACTTAAG 560
|||
320 TGAATTCAGCTGAATCTGAAGTGAAGGAAATTGTCGCAAGATACAGAACTTAAG 379
|||
561 CGAAGTTGAGACCATCAAAAATGTCACAAAGC 593
|||
380 CGAAGTTGAGACCATCAAAAATGTCACAAAGC 412
|||

RESULT 3
AF112150 1250 bp mRNA linear PLN 19-SEP-2001
LOCUS Zea mays MADS box protein 3 (mads3) mRNA, complete cds.
DEFINITION
ACCESSION AF112150

VERSION	AF112150.1	GI:12002140
KEYWORDS	Zea mays.	
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.	
ORGANISM	1 (bases 1 to 1250)	
REFERENCE	Heuer,S., Hansen,S., Bantini,J., Bretschneider,R., Kranz,E., Lortz,H. and Dresselhaus,T.	
AUTHORS	The maize MADS box gene ZmMADS3 affects node number and spikelet development and is co-expressed with ZmMADS1 during flower development, in egg cells, and early embryogenesis	
TITLE	Plant Physiol. 127 (1), 33-45 (2001)	
JOURNAL	2143/929	
MEDLINE	2143/929	
PUBMED	11553732	
REFERENCE	2 (bases 1 to 1250)	
AUTHORS	Heuer,S., Dresselhaus,T. and Lortz,H.	
TITLE	Maize MADS box genes expressed in egg cells	
JOURNAL	Unpublished	
REFERENCE	3 (bases 1 to 1250)	
AUTHORS	Heuer,S., Dresselhaus,T. and Lortz,H.	
TITLE	Submitted Submission	
JOURNAL	Submitted (09-DEC-1998) Centre for Applied Molecular Plant Biology	
REFERENCE	AMP II, University of Hamburg, Ohnhorststrasse 18, Hamburg 22609, Germany	
FEATURES	Location/Qualifiers	
source	1..1250	
	/organism="Zea mays"	
	/strain="A188"	
	/db_xref="taxon:4577"	
	/cell_type="egg"	
gene	1..1250	
	/gene="mads3"	
	/note="expressed in immature male and female flowers, egg cells and nodes"	
	70..882	
CDS	/gene="mads3"	
	/codon_start=1	
	/product="MADS box protein 3"	
	/protein_id="AAG43200.1"	
	/db_xref="GI:12002141"	
	/translation="MGRGKVKQLKREINQVTFSSKRNLLKKAHEISVLCDAEVA VIVSPKAKLREYASDSRMDKILERYEYSIAEKLISAESSEGNWCHERYRKAKAKI ETIQRCHKLMDLEDLSINPELQOLEQOLSLKHSIRSRSHLMAESIQLOKERS LOENRKHLMKELSEROKAVASRQOOQOVNDQOVOTSSSSSPMMDQOQGLE PPNVCPPPLSISGRGEVMAAAGQOLPPPOAQPOLRIAGLPPMMLSHLMA"	
BASE COUNT	361 a	295 c 352 g 242 t
GCIN		
Query Match	51.0%; Score 302.6; DB 8; Length 1250;	
Best Local Similarity	93.7%; Pred. No. 4.6e-62;	
Matches	314; Conservative	0; Mismatches 21; Indels 0; Gaps 0;
QY	259	GGATATGGGTGCGCGCAAGGTGACGCTGAAGCGATAGAAACAAGATAATCGGACAGT 318
DB	66	GAAATGGGGGCGCGCAAGGTGACGCTGAAGCGATAGAAACAAGATAAATCGGACAGT 125
QY	319	GACCTTCCCAAGCGCGCAACGGGCTCCTGAAGAAGCGACGATCTCGCTCTG 378
DB	126	GACCTTCTCCCAAGCGCGCAACGGGCTCTGAAGAAGCGACGATCTCGCTCTG 185
QY	379	TGACGCGAGGTGCGCGTCATGCTTCTCCGCCAAGCAAGCTCTATGAGTAGCGCAC 438
DB	186	CGACGCGAGGTGCGCGTCATGCTTCTCCGCCAAGCAAGCTCTATGAGTAGCGCTC 245
QY	439	CGACTCCGACGTGACAAAATTTCTTGAACGTTATGAGCGCTATCTTATGCTGAAGGC 498
DB	246	CGACTCCGACGTGACAAAATTTCTTGAACGTTATGAGCGCTATCTTATGCTGAAGGC 305
QY	499	TCTTATTTACGCTGAATCTGAAGAAGGAGGAAATTGGTGCACGAAATCAGGAAACTTAA 558
DB	306	TCTTATTTACGCTGAATCTGAAGAAGGAGGAAATTGGTGCACGAAATCAGGAAACTTAA 365

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
LOCUS AR042842	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
DEFINITION	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
ACCESSION	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
VERSION	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
KEYWORDS	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
SOURCE	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
ORGANISM	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
REFERENCE	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
AUTHORS	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
TITLE	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
JOURNAL	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
FEATURES	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
BASE COUNT	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
ORIGIN	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
Query Match	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
Best Local Similarity	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
Matches 316; Conservative	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
50.7%; Score 300.4; DB 6; Length 1345;	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
92.4%; Pred.No.1.6e-61;	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
0; Mismatches 26; Indels 0; Gaps 0;	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
349 a 373 c 358 g 265 t	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
1.1345	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
/organism="unknown"	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
Location/Qualifiers	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
1.1345	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
252 GAAATCAGATATGATGGTTCGCGCGCAAGTGTGCTGAGCGGATGAGAACAAATTAATC 311	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
138 GCAACAAGCGCATGGGCGCGCGCAAGTATGACGTGGAAGCGGATGAGAACAAATTAAC 197	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
312 GGCAGGTGACCTTCTCCAAAGCGCGCAAGCGGCTCTGGAAGAGCGCGCAGATCTCG 371	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
198 GGCAGGTGACCTTCTCCAAAGCGCGCAAGCGGCTCTGGAAGAGCGCGCAGATCTCG 257	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
372 TCCCTGTGACGCGGAGGTGCGCGCTCATGCTCTCTCCCAAGGCAAGCTCATGAGT 431	Sequence 7 from patent US 5811536.	AR042842	1	GI:5963338	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanoftsky,M.F.
258 TCCCTGTGACGCGGAGGTGCGCGCTCATGCTCTCTCTCCCAAGGCAAGCTCATGAGT 317	Sequence 7 from patent US 5811536.	AR042842	1						

BASE COUNT	349	a	373	c	358	g	265	t
ORIGIN	/organism="unknown"							

Query Match	50.7%;	Score 300.4;	DB 6;	Length 1345;
Best Local Similarity	92.4%;	Pred. No. 1.6e-61;		
Matches 316;	Conservative 0;	Mismatches 26;	Indels 0;	Gaps 0;

QY	252	GAATATCAGAAATATGGATCGCGCAGAGTGCACCTAGAGGGATATAGAAACAAGATTAATC	311
Db	138	GCAACAAGCCGATGGGGCGCGGCMAAGTACAGCTGAGCGGATAGGAACAAGATTAAC	197
QY	312	GGCAGGTGACTTCTTCCAAAGCCCGCAAGGGCTCTGAAGAAAGCGCACGATCTCG	371
Db	198	GGCAGGTGACTTCTTCCAAAGCCCGCAAGGGCTCTGAAGAAAGCGCACGATCTCG	257
QY	372	TCCTGTGACCGCGAGGTGCGCGATCGTCTTCCGCCAAAGCAAGCTCTTAGT	431
Db	258	TCCTGTGAGTATCCGAGGTGCGCGATCGTCTTCTTCCGCCAAAGGCAAGCTCTTAGT	317
QY	432	ACGCCACCGACTTCAGCATGGAACAATTTCTTGAACGTATAGAGGCTACTTATGCTG	491
Db	318	ACGCCACCGACTTCAGCATGGAACAATTTCTTGAACGTATAGAGGCTACTTATGCTG	377
QY	492	AAAAAGCTTTATTTTCAGCTGAATCTGAAGTAGAGGAATTTGTCGCCAGATACAGA	551
Db	378	AAAAAGCTTTATTTTCAGCTGAATCTGAAGTAGAGGAATTTGTCGCCAGATACAGA	437
QY	552	AACTTAAGCGGAAGTATGACATTCACCAAAATATGTCACAGC	593
Db	438	AACTTAAGCGCAAAATATGACATTCACCAAAATATGTCACAGC	479

RESULT 6	
AR111350	
LOCUS	
AR111350	1345 bp
	DNA
	linear
	PAT 14-FEB-2001

DEFINITION	Sequence 7 from patent US 6127123.
ACCESSION	AR111350
VERSION	AR111350.1 GI:12828198
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 1345)
TITLE	Yanofsky, M.F. Cautilflower floral meristem identity genes and methods of using same
JOURNAL	Patent: US 6127123-A 7 03-OCT-2000;
ATTUES	Location/Qualifiers
source	1..1345 /organism="unknown"
BASE COUNT	349 a 373 c 358 g 265 t
ORIGIN	
Query Match	50.7%; Score 300.4; DB 6; Length 1345;
Best Local Similarity	92.4%; Pred. No. 1,6e-61;
Matches 316; Conservative	0; Mismatches 26; Indels 0; Gaps 0

Oy	252	GAAATCAGATATGCGTCGCGGCAAGTGACGTGAAGCGAGATAGAGAA	CAAGATAAATC	311
Db	138	GCAACAAAGCGATGGGGCGGGCGCAAGGTACGCTGAAGGGATAGGAAC	CAAGATTAATCC	197
Oy	312	GGCAGGTGACCTTCTCCAAAGCGCGCAACGGGCTCCTGAAAGAGCGCA	CGAGATCTCG	371
Db	198	GGCAGGTGACCTTCTCCAAAGCGCGCAACGGGCTCCTCAAGAAAGCGCA	CGAGATCTCG	257
Oy	372	TCTCTGTACGGGGAGGTGCGCGTCATCGTCTTCCCCAAAGGCAAGCTT	ATAGAGT	431
Db	258	TCTCTGTGCAATGCCAGAGGTGCGCGTCATCGTCTTCTCCCCAAAGGCA	AGCTTACGAGT	317
Oy	432	ACGCCACGACTCCAGCATGAGCAAAATCTTGAACGTTATGAGCGCTA	CTCTATAGCTG	491
Db	318	AGGCCACCGACTTCCGCAATGAGCAAAATCTTGAACGTTATGAGCGAT	TCTCTATAGCTG	377

Oy	492	AAAAGCTTTATTTTCAGCTGAATTGAAAGTGAGGGAAATTTGTGCACCAATAACAGA	51
Db	378	AAAAGCTTTATTTTCAGCTGAATTGAAAGTGAGGGAAATTTGTGCACCAATAACAGA	437
Oy	552	AACCTAAGGCGAAGTGTGACCATAACAAAAATGTACAAC	593
Db	438	AACCTAAGGCCAAATGTGACCATCAAAAAATGTCCAAC	479

RESULT 7	AR200417	1345 bp	DNA	linear	PAT 20-APR-2002
LOCUS	AR200417				
DEFINITION	Sequence 7 from patent US 6355863.				
ACCESSION	AR200417				
VERSION	AR200417.1	GI:20250491			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1345)				
TITLE	Yanofsky,M.F.				
JOURNAL	Seed plants exhibiting inducible early reproductive development and				
FEATURES	methods of making same				
	Parent: US 6355863-A 7 12-MAR-2002;				
	1. location/Qualifiers				
	1. 1345				
	/organism="unknown"				
BASE COUNT	349 a	373 c	358 g	265 t	
ORIGIN					

Query Match:	50.7%	Score 300.4:	DB 6:	Length 1345:
Best Local Similarity:	92.4%	Pred. No. 1.ee-61:		
Matches 316:	Conservative 0:	Mismatches 26:	Indels 0:	Gaps 0:

QY	252	GAATTCAGGATATATGGTCCGGCGCAAGGCGACGCTGGAAGCGGATATGAGAAACAAGATTAATC	311
Db	138	GCAACAAGCGCATGGGGGGCGCGCAAGGATACGCTGAAGCGGATAGAGAAACAAGATTAATCC	197
QY	312	GGCAGAGTACCTTCTCCCAAGCGCGCAACGGGCTCTTGAAAGAGCGCACGAGATCTTCCG	371
Db	198	GGCAGGTACCTTCTCCCAAGCGCGCGGAAGCGGCTGCTCTCAAGAGCGCACGAGATCTTCCG	257
QY	372	TCTCTGTGACGCGGAGGTCCGCGTCATCGTCTTCTCCGCCAAAGCAAGCTTTATGAGT	431
Db	258	TCTCTGTGAGTCCGAGGTTGCGCGTCATCGTCTTCTCCGCCAAGGCAAGCTCTACGAGT	317
QY	432	ACGCCACCGACTCCAGCATGACAAAAATTTCTTGAACGTTATGAGCGCTTACTTATGCTG	491
Db	318	ACGCCACCGACTCCCGCATGACAAAAATTTCTTGAACGTTATGAGCGGATTTCTATGCTG	377
QY	492	AAAAAGCTTATTTCACTGAAATCTGAAATGTGAGGGGAAATTGGTCCACGAAATACAGA	551
Db	378	AAAAAGCTTATTTCACTGAAATCTGAAATGTGAGGGGAAATTGGTCCACGAAATACAGA	437
QY	552	AACCTTAAGCGAAGTTGAGCCATACAAAATGTCAACAG	593
Db	438	AACCTTAAGCGCAAAATTTGAGCCATACAAAATGTCCACAGC	479

RESULT 8
MZEMADSD
LOCUS MZEMADSD 1345 bp mRNA linear PLN 16-MAY-1996
DEFINITION Zea mays MADS-box protein (ZAP1) mRNA, complete cds.
ACCESSION L46400
VERSION L46400.1 GI:939784
KEYWORDS MADS box protein.
SOURCE Zea mays CDNA to mRNA.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1345)
REFERENCE

AUTHORS Mena, M., Mandel, M.A., Lerner, D.R., Yanofsky, M.F. and Schmidt, R.J.
 TITLE A characterization of the MADS-box gene family in maize
 JOURNAL Plant J. 8 (6), 845-854 (1995)
 MEDLINE 96132144
 PUBMED 8580958

FEATURES
 source Location/Qualifiers

1..1345
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 /db_xref="taxon:4577"
 /map="chromosome 3D2L"
 /cissue_type="female inflorescence"
 /dev_stage="immature ear"
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 /gene="ZAP1"
 149..970
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 /product="MADS box protein"
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 /db_xref="GI:939785"
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 VIVFSPKGLYEATDSMDKILERYERYVAEKALISAESSEGNWCHERYKTKIKTI
 EITOKCHLMGDELSLNPKLEQLEQOLDSLKHIRKSHMAESI SELOKERS
 LOENKALOEKLAERKAVASRQ000000VQMDQTHAQOTSSSSSSSMHRODQGL
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BASE COUNT 349 a 358 g 265 t
 ORIGIN

Query Match 50.7%; Score 300.4; DB 8; Length 1345;
 Best Local Similarity 92.4%; Pred. No. 1.6e-61;
 Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 252 GAAATAGATATAGGTCGCGGCAAGTGCAGTGAAGCGGATAGAGAAATTAATC 311
 DB 138 GCACACAGCGATGGGGCGGCGAAGTACGTGAAGCGATAGACACATTAACC 197
 QY 312 GCGAGTGAACCTTCTTCAAGCGCGGCAACGGGCTCTTGAAGAGCGCAAGATCTCG 371
 DB 198 GCGAGTGAACCTTCTTCAAGCGCGGCAACGGGCTCTTGAAGAGCGCAAGATCTCG 257
 QY 372 TCCTGTGACGGGAGGTGCGCGTATGCTTCTTCCCAAGGCAAGCTTATAGT 431
 DB 258 TCCTGTGACGGGAGGTGCGCGTATGCTTCTTCCCAAGGCAAGCTTATAGT 317
 QY 432 ACGCCACGACTCCAGATGACCAAAATCTTGAAGCTTATGAGCGCTATGCTG 491
 DB 318 ACGCCACGACTCCAGATGACCAAAATCTTGAAGCTTATGAGCGCTATGCTG 377
 QY 492 AAAAGGCTTTATTTAGCTGAATCTGAAGTGAAGGAAATGGTCCAGATACAGA 551
 DB 378 AAAAGGCTTTATTTAGCTGAATCTGAAGTGAAGGAAATGGTCCAGATACAGA 437
 QY 552 AACTTAAGCGGAAGATTGAGACCATCAAAAATGTCAACAGC 593
 DB 438 AACTGAAGGCCAAATTAAGACCATCAAAAATGTCAACAGC 479

RESULT 9
 SB032110 1186 bp mRNA linear PLN 24-MAR-1997
 LOCUS Sorghum bicolor putative MADS box protein (SBMADS2) mRNA, partial
 DEFINITION cds.
 ACCESSION U32110.1 GI:1905933
 VERSION U32110.1
 KEYWORDS Sorghum bicolor.
 SOURCE Sorghum bicolor.
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoidae; Andropogonae; Sorghum.
 REFERENCE 1 (bases 1 to 1186)
 Greco, R., Stagi, L., Colombo, L., Angenent, G.C., Sari-Gorla, M. and
 Pe, M.E.

TITLE MADS box genes expressed in developing inflorescences of rice and
 sorghum
 JOURNAL Mol. Genet. 253 (5), 615-623 (1997)
 MEDLINE 97218034
 PUBMED 9065695

REFERENCE 2 (bases 1 to 1186)
 Greco, R., Stagi, L., Colombo, L., Pe, M.E. and Angenent, G.C.
 Direct Submission
 JOURNAL Submitted (21-JUN-1995) Raffaella Greco, Università di Milano,
 Genetica e Biologia dei Microorganismi, Via Celoria 26, Milano, MI,
 Italia, 20133

FEATURES
 source Location/Qualifiers

1..1186
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 /db_xref="taxon:4558"
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 /gene="SBMADS2"
 /note="putative MADS box protein"
 /codon_start=3
 /product="MADS box protein"
 /protein_id="AB0181.1"
 /db_xref="GI:1905934"
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 SPKGLYEATDSMDKILERYERYVAEKALISAESSEGNWCHERYKTKIKTI
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 NKALOEKLAERKAAASRQ0000GANGPDPBPDKLITVILHDEAGSAGAASTKHM
 LPAADRER"

BASE COUNT 334 a 300 c 313 g 239 t
 ORIGIN

Query Match 49.3%; Score 292.2; DB 8; Length 1186;
 Best Local Similarity 94.4%; Pred. No. 1.4e-59;
 Matches 303; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 273 GCAAGTGCAGCTGAAGCGGATAGAGAAATTAATTCGCGAGTGAACCTTCTCAAGC 332
 DB 1 GCAGTGCAGCTGAAGCGGATAGAGAAATTAATTCGCGAGTGAACCTTCTCAAGC 60
 QY 333 GCGCAAGGCTCTTGAAGAGCGCAAGATCTCGTCTTGTACCGGAGTGC 392
 DB 61 GCGCAAGGCTCTTGAAGAGCGCAAGATCTCGTCTTGTACCGGAGTGC 120
 QY 393 CGGTATGCTTCTTCCCAAGGCAAGCTTATGATGAGCCACGATCCGATG 452
 DB 121 CGGTATGCTTCTTCCCAAGGCAAGCTTATGATGAGCCACGATCCGATG 180
 QY 453 ACAAAATCTTGAAGCTTATGAGCGCTACTCTTATGTAAGAGCTTTATTTAGCTG 512
 DB 181 ACAAAATCTTGAAGCTTATGAGCGCTACTCTTATGTAAGAGCTTTATTTAGCTG 240
 QY 513 AATCTGAAGTGAAGGAAATTTGTCACGAATACAGAAAATTAAAGCGAAGATTGAGA 572
 DB 241 AATCTGAAGTGAAGGAAATTTGTCACGAATACAGAAAATTAAAGCGAAGATTGAGA 300
 QY 573 CCATACAAAATGTCAACAGC 593
 DB 301 CCATACAAAATGTCAACAGC 321

RESULT 10
 AF058698 1285 bp mRNA linear PLN 27-DEC-1999
 LOCUS Oryza sativa MADS15 protein mRNA, complete cds.
 DEFINITION AF058698
 ACCESSION AF058698
 VERSION AF058698.1 GI:6606071
 KEYWORDS Oryza sativa.
 SOURCE Oryza sativa.
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 1289)	Kojima, M., Sasaki, T., Nozue, M. and Shioiri, H.	A gene controlling for branching of plants, a vector containing said gene, an microorganism containing said vector and a method for controlling of branch of plant	Patent: WO 0114559-A 1 01-MAR-2001;	
	KUMIDA CHEMICAL INDUSTRY CO LTD, MINO KOJIMA, TAKUJI SASAKI, ASAYUKI			
	NOZUE, HIDEHARI SHIOIRI			
	OS	Oryza sativa (rice)		
	FN	WO 0114559-A/1		
	PD	01-MAR-2001		
	PR	18-AUG-2000 WO 2000JP005537		
	PR	19-AUG-1999 JP 99P 232318		
	PI	MINO KOJIMA, TAKUJI SASAKI, MASAYUKI NOZUE, HIDEHARI SHIOIRI		
		C12N15/29, A01H5/00		
FEATURES	source	location/Qualifiers	location/Qualifiers	
		1..1289		
		/organism="Oryza sativa"		
		/db_xref="taxon:4530"		
BASE COUNT	354 a	316 c	337 g	282 t
ORIGIN				
Query Match	47.8%;	Score 283.2;	DB 6;	Length 1289;
Best Local Similarity	89.0%;	Pred. No. 2.1e-57;		
Matches 306;	Conservative	0;	Mismatches 38;	Indels 0;
				Gaps 0;
Oy	250	GCGAATCAGGATATGAGGTCGCGGCAAGTGCAGCTGAAGCGATAGAGCAAGATPAA	309	
Db	112	GCGAGCGGCGAGATGGGCGCGGAGAGTGCAGCTGAAGCGATAGAGCAAGATPAA	171	
Oy	310	TCGGCAGTGCACCTTCTCCAAAGCGCGCAACGGCTCTTGAAGGCGCAGAGATTC	369	
Db	172	CAGGCAAGTACGTTCTCCAAAGAGAGAAATGATTCCTGAAGAGCGCAGAGATTC	231	
Oy	370	CGTCTCTGTGAGCGCGAGGTCGCGGTCATCGTCTTCTCCCAAGCGAAGCTCTATGA	429	
Db	232	CGTCTCTGTGAGCGCGCAGAGTTCGCGGTCATCGTCTTCTCCCAAGCGAAGCTCTACGA	291	
Oy	430	GTACGCCACGACCTCCGACATGACCAAAATCTTGAAGCTATAGGCGCTACTCTTATGC	489	
Db	292	GTACGCCACGACCTCCGACATGACCAAAATCTTGAAGCTTATAGGCGCTATTCATATGC	351	
Oy	490	TGAAAAGGCTCTTATTTCAAGTGAATCTGAAAGTAGAGGAAATGGTGCCAGAAATACAG	549	
Db	352	TGAAAAGGCTCTTATTTCAAGTGAATCTGAAAGTAGAGGAAATGGTGCCAGAAATACAG	411	
Oy	550	GAAACTTAAGCGCAAGATTGAGACCATACAAAAATGTCACAAGC	593	
Db	412	GAAACTTAAGCGCAAGATTGAGACCATACAAAAATGTCACAAGC	455	
RESULT 12				
AB003325		1289 bp	mRNA	linear
LOCUS	Oryza sativa (japonica cultivar-group)			PLN 21-MAR-2007
DEFINITION	Oryza sativa (japonica cultivar-group) mRNA for MADS box-like protein, complete cds, clone:E31864.			
ACCESSION	AB003325			
VERSION	AB003325.1			
KEYWORDS	MADS box-like protein.			
SOURCE	Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) panicle at pre-meiotic stage cDNA to mRNA, clone_1ib:cDNA panicle at pre-meiotic stage clone:E31864.			
ORGANISM	Oryza sativa (japonica cultivar-group)			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.			
REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	Shinozuka, Y., Yamamoto, K. and Sasaki, T.			

TITLE Characterization of rice MADS box-like genes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1289)
AUTHORS Sasaki, T.
TITLE Direct Submission
JOURNAL Submitted (23-APR-1997) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program, Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@abr.affrc.go.jp, Tel:0298-38-7441,
Fax:0298-38-7468)

FEATURES
source Location/Qualifiers
1..1289
/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="E31864"
/issue_type="panicle at pre-meiotic stage"
/clone_id="cdna panicle at pre-meiotic stage"
125..928
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/protein_id="BA8183.1"
/db_xref="GI:5295984"

CDS
BASE COUNT 354 a 316 c 337 g 282 t
ORIGIN

Query Match 47.8%; Score 283.2; DB 8; Length 1289;
Best Local Similarity 89.0%; Pred. No. 2.1e-57;
Matches 306; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

OY 250 GCGAATTCAGATATGGTCGCGCAAGTGCCTGAAAGCGATGAGAACAGATATA 309
DB 112 GCGAGCGCGAGATGGCGCGGGAAGGTGCGAGTGAAGCGATGAGAACAGATCA 171
OY 310 TCGGAGGTGACCTTCCCAAGCGCGCAAGCGCTCCGGAAGAGCGCAGAGATCTC 369
DB 172 CAGGCAAGTGAAGCTTCCCAAGGAGGATGATGCTGAAGAGCGCAGAGATCTC 231
OY 370 CGTCTCTGTGACGCGGAGGTGCGCTCATGCTCTTCTCCCAAGGCAAGCTTATGA 429
DB 232 CGTCTCTGTGACGCGGAGGTGCGCTCATGCTCTTCTCCCAAGGCAAGCTTATGA 291
OY 430 GTACGCCACGACTCCAGCATGAGCAAAATCTTGAAGCTTATGAGCGCTACTCTTATGC 489
DB 292 GTACGCCACGACTCCAGCATGAGCAAAATCTTGAAGCTTATGAGCGCTACTCTTATGC 351
OY 490 TGAAGAAGCTCTTATTTAGCTGTAATCTGAAGTGAAGGAAATGGTGCACGATACAG 549
DB 352 TGAAGAAGCTCTTATTTAGCTGTAATCTGAAGTGAAGGAAATGGTGCACGATACAG 411
OY 550 GAAACTTAAGCGCAAGATTGAGACCATACAAAATGTCCACAAGC 593
DB 412 GAAACTTAAGCGCAAGATTGAGACCATACAAAATGTCCACAAGC 455

RESULT 13
BD005239 standard; DNA; PLN; 1289 BP.
ID BD005239
XX BD005239;
AC
SV BD005239.1
XX
DT 08-FEB-2002 (Rel. 70, Last updated, Version 1)
XX
DE A gene controlling for branching of plants, a vector containing said gene,
an microorganism containing said vector and a method for controlling of

DE branch of plant.
XX
XX JP 03075374-T/1.
XX
OS Oryza sativa
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae;
OC Oryzae; Oryza.
XX
XX
RN [1]
RP 1-1289
RA Kojima M., Sasaki T., Nozue M., Shioiri H.,
RT "A gene controlling for branching of plants, a vector containing said gene,
RT an microorganism containing said vector and a method for controlling of
RT branch of plant";
RL Patent number JP03075374-T/1, 16-FEB-2001.
RL KUMARI CHEMICAL INDUSTRY CO LTD, MINO KOJIMA, TAKUJI SASAKI, ASAYUKI NOZUE,
RL HIDEHARI SHIOIRI.
XX

OS Oryza sativa (rice)
CC PN JP 03075374-T/1
CC PD 16-FEB-2001
CC PF 18-AUG-2000 JP 200005537
CC PR 19-AUG-1999 JP 99P 232318
CC PI MINO KOJIMA, TAKUJI SASAKI, MASAYUKI NOZUE, HIDEHARI SHIOIRI
CC PC C12N15/29, A01H5/00
CC CC
CC FH Key Location/Qualifiers
CC FT 1..1289
CC FT source /db_xref="taxon:4530"
CC FT /organism="Oryza sativa"

Sequence 1289 BP; 354 A; 316 C; 337 G; 282 T; 0 other;
Query Match 47.8%; Score 283.2; DB 23; Length 1289;
Best Local Similarity 89.0%; Pred. No. 2.1e-57;
Matches 306; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

OY 250 GCGAATTCAGATATGGTCGCGCAAGTGCCTGAAAGCGATGAGAACAGATATA 309
DB 112 GCGAGCGCGAGATGGCGCGGGAAGGTGCGAGTGAAGCGATGAGAACAGATCA 171
OY 310 TCGGAGGTGACCTTCCCAAGCGCGCAAGCGCTCCGGAAGAGCGCAGAGATCTC 369
DB 172 CAGGCAAGTGAAGCTTCCCAAGGAGGATGATGCTGAAGAGCGCAGAGATCTC 231
OY 370 CGTCTCTGTGACGCGGAGGTGCGCTCATGCTCTTCTCCCAAGGCAAGCTTATGA 429
DB 232 CGTCTCTGTGACGCGGAGGTGCGCTCATGCTCTTCTCCCAAGGCAAGCTTATGA 291
OY 430 GTACGCCACGACTCCAGCATGAGCAAAATCTTGAAGCTTATGAGCGCTACTCTTATGC 489
DB 292 GTACGCCACGACTCCAGCATGAGCAAAATCTTGAAGCTTATGAGCGCTACTCTTATGC 351
OY 490 TGAAGAAGCTCTTATTTAGCTGTAATCTGAAGTGAAGGAAATGGTGCACGATACAG 549
DB 352 TGAAGAAGCTCTTATTTAGCTGTAATCTGAAGTGAAGGAAATGGTGCACGATACAG 411
OY 550 GAAACTTAAGCGCAAGATTGAGACCATACAAAATGTCCACAAGC 593
DB 412 GAAACTTAAGCGCAAGATTGAGACCATACAAAATGTCCACAAGC 455

RESULT 14
AF345911 1347 bp mRNA linear PLN 02-OCT-2001
LOCUS AF345911
DEFINITION Oryza sativa MADS-box protein FDRMADS3 mRNA, complete cds.
ACCESSION AF345911

VERSION	AF345911.1	GI:15824794
KEYWORDS	Oryza sativa.	
SOURCE	Oryza sativa	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaceae; Oryza.	
REFERENCE	1 (bases 1 to 1347)	
AUTHORS	Gao Z., Chen R., Jia H. and Sun C.	
TITLE	Direct Submission	
JOURNAL	Submitted (06-FEB-2001) Biochemistry, Fudan University, 220 Handan Road, Shanghai 200433, P.R. China	
FEATURES	Location/Qualifiers	
source	1..1347	
CDS	/organism="Oryza sativa"	
	/db_xref="taxon:4530"	
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	/codon_start=1	
	/product="MADS-box protein FDRMADS3"	
	/protein_id="AAI09473.1"	
	/db_xref="gi:15824795"	
	/translation="MGKGVOLIKRIENSMNRPVPSKRNGILKKAHISVICIAAEVA ALVESPKLKYEAATSDMSMDKLPRYSYSAEKLISABESSENMCHERYKAKA ETIQCKHLMGEDIESLNLUKELOOLEQOLSSLKHTIRSKSHMLBSISELQKERS LOEKNAJQKELVERQKNVGQOVGDVDQVOQAQAOPOAQTSFFPFMLDQQQ LSPNNICYPPVMGQRNDAAARRMRKPCNFRIIGFPPMMLSTFYA"	
BASE COUNT	376 a 313 c 354 g 304 t	
ORIGIN		
Query Match	47.5%; Score 281.6; DB 8; Length 1347;	
Best Local Similarity	88.7%; Pred.No.56-57; 39; Indels 0; Gaps 0;	
Matches	305; Conservative 0; Mismatches 39; Indels 0; Gaps 0;	
Oy	250 GCGAATACAGATTATGGTCTCCGCCGAGAAGTGCAAGTCGAAGCCGATAGAACAAATATAA 309	
Dd	112 CGAGACGGGAGAGATGGGGCGGGGGAAGGTGCAGCTGAAGCGGATAGAGAACTCATGA 171	
Oy	310 TCGGCAAGTAGACTCTTCTCCAAGCGCCGCAACGGGCTCCTGAAGAAAGCGCCAGAAATCTC 369	
Dd	172 CCGGAGAGTAGAGTTCTCCMAAGAGAGATGATGTCTGAAGAAAGGCGCACAGATCTC 231	
Oy	370 GCCTCTGTGACGGGAGAGTGGCGGTCATCGTCTTCTCCCCCAAAGCGAAGCTTATGA 429	
Dd	222 GGTCTCTTCGACGCCGAGAGTGGCGGCATCTCTTCTCCCCCAAAGCGAAGCTTATGA 291	
Oy	430 GTAGCCACCGAATCCAGCATGAGCAAAATTTGTAACGTTATGAGCGCTACTTTATGC 489	
Dd	292 GTAGCCACTGACTCCAGAGTGAAGAAAATCCTTGAACGTTATGAGCGCTATTCATATGC 351	
Oy	490 TGAAGAAGCTTATTTACGTGATTCGTAATCGAAGTGAAGGAAATTGTCACAGATATACG 549	
Dd	352 TGAAAAAGCTCTTATTTACGTGATTCGTAATCGAAGTGAAGGAAATTGTCACAGATATACG 411	
Oy	550 GAACCTTAAGCGCAAGATTGAGACCATACAAAAATGTCAACAAGC 593	
Dd	412 GAAGCTTAAGCAAGATTGAGACCATACAAAAATGTCAACAAC 455	
RESULT 15	AB007504	1161 bp mRNA linear JUN 08-MAY-2002
LOCUS	AB007504	Triticum aestivum TAMADS#11 mRNA for MADS box transcription factor,
DEFINITION	complete cds.	
ACCESSION	AB007504	GI:3688588
VERSION	TAMADS#11; MADS box transcription factor.	
KEYWORDS	Triticum aestivum young spike cDNA to mRNA.	
SOURCE	Triticum aestivum	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.	
REFERENCE	Murai,K., Murai,R., Takumi,S. and Ogihara,Y.	

	TITLE	Cloning and characterization of cDNAs corresponding to the wheat MADS box genes (in) A.E. Slinkard (Ed.) ; PROCEEDINGS OF THE 9TH INTERNATIONAL WHEAT GENETICS SYMPOSIUM: 89-94; University Extension Press, Saskatchewan, Canada (1998)					
JOURNAL	AUTHORS	Murai, K., Murai, R., Takumi, S. and Ogihara, Y.					
TITLE	AUTHORS	cDNA cloning of three MADS box genes in wheat (Accession Nos. AB007504, AB007505 and AB007506) (PCR98-159) Plant Physiol. 118, 330 (1998)					
JOURNAL	REFERENCE	Murai, K., Takumi, S., Koga, H. and Ogihara, Y.					
AUTHORS	REFERENCE	Pistillody, homeotic transformation of stamens into pistil-like structures, caused by nuclear-cytoplasm interaction in wheat Plant J. 29 (2), 169-181 (2002)					
TITLE	REFERENCE	Murai, K. Direct Submision Submitted (22-SEP-1997) Koji Murai, Fuku Prefectural University, Department of Bioscience, 4-1-1, kengo-jima, Matsuyaka-cho, Yoshida-gun, Fukui 910-1195, Japan [E-mail: murai@fpu.ac.jp, Tel:0776-61-6000(ex.3618), Fax:0776-61-6015] Location/Qualifiers					
FEATURES	SOURCE	1..1161 /organism="Triticum aestivum" /db_xref="taxon:4565" /tissue_type="Young spike"					
	gene	1..1161 /gene="TaMADS#11"					
	CDS	75..809 /gene="TaMADS#11" /codon_start=1 /product="MADS box transcription factor" /protein_id="BAJ3457.1" /db_xref="GI:3688589"					
	polyA_site	translaction="MGGRKVLKRLEKNINQVTSKRSGILKKAHESIVCDAEV LIIITGKLVEFTSESCMDKILERIEYSVAEKLVSESETIQGWCHERYLKLRK ETIKOCNHLNGEDLESINLKELOQLBESLSLHISRKQIWHESISLQKER LOENRKYLMKELIVEKOQAQQDPTQTSSTSSSPFWRDAPPAALASIHPPAAEE AGDAVQPQAPPRTGLPLMVSHING" 1161 /gene="TaMADS#11" /note="20 a nucleotides"					
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Query Match	Best Local Similarity	44.6% Score 264.6; DB 8; Length 1161;					
Matches	Conservative	Pred No. 5.8e-53; Mismatches 44; Indels 0; Gaps 0					
Db	259	GGATTGCGGTCCGGCAAGTGTCACCTGAAGCGGATAGAGAACAGATAATCGCAGGT 318					
Qy	71	GGAGATGGGGCGCGGGAAGTGTCACACTGAAGCGGATCGAGAACAGATCAACGGCAGGT 130					
Db	319	GACCTTTCTCCAAGCCCCGCCCAAGGGCTCTTAAGAAGGGCGACGAGATTCCTGCTCTG 378					
Qy	131	GACCTTTCTCCAAGCCCCGCCCTCGGGGCTGTCAAGAAGGGCGACGAGATTCGCTCTG 190					
Db	379	TGACCGGAGGTCGCGGTCATCATGCTTTCTCCCCCAAAGGCAGCTCTATAGTACGCCAC 438					
Qy	191	CGACCGCAGGTCGCGGCTCATCATCTTTCTCCACCAAGGAAGAGCTTACAAGATTCTCCAC 250					
Db	439	CGACTCCAGCATGACCAAAATTTCTGAACGTTATGAGCGCTTACTTTATGCTGAAGAAGC 498					
Qy	251	CGAGTCATGATGACCAAAATTTCTGAACGCTATGAGCGCTTACTTTATGCGAAAAAGGT 310					
Db	499	TCTTATTTACGCTGAATCGAAGGAGGGAATGTCGCCAGATATACGGAATCTTAA 558					
Qy	311	TCTCGTTCAAGTGAATCTGAATATTCAGGGAATGCTGTCAAGATATAGGAATCTGA 370					

Mon Jun 30 09:38:35 2003

us-10-020-338-8.rge

Page 9

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QY      559  GGGCAAGATTGAGACCATACAAAATGTCTCAGC  593
          |||||  |||||  |||||  |||||  |||||
Db      371  GGGCAAGTTGAGACATACAGAAATGTCAAAGC  405

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Search completed: June 29, 2003, 07:50:49
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 PR 30-APR-1999; 99US-0131449.
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PR 29-OCT-1999; 99US-0162142.

Query Match 51.0%; Score 302.6; DB 21; Length 496;
Best Local Similarity 93.7%; Pred. No. 5.3e-76;
Matches 314; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 259 GGATATGCGTCCGCGGCAAGCTGAGTGAAGCGATAGAAACAAGATAAATCGCAGGT 318
DB 65 GAAGATGGGGCCGCGCAAGCTGAGTGAAGCGATAGAAACAAGATAAATCGCAGGT 124
QY 319 GACCTTCTCAAGCGCGCAAGCGGCTCTGAAGAGCGCGAGATCTCGCTCTTG 378
DB 125 GACCTTCTCAAGCGCGCAAGCGGCTCTGAAGAGCGCGAGATCTCGCTCTTG 184
QY 379 TGACCGGAGGTCGCGCTGATGCTTTCTCCCAAGGCAAGCTCTATGATGAGCCAC 438
DB 185 CGAGCGCGAGGTCGCGCTGATGCTTTCTCCCAAGGCAAGCTCTATGATGAGCCAC 244
QY 439 CGACTTCAGCATGAGCAAAATTTCTGAAGCTTATGAGGCTTATGATGAGGCA 498
DB 245 CGACTTCAGCATGAGCAAAATTTCTGAAGCTTATGAGGCTTATGATGAGGCA 304
QY 499 TCTTATTTCAAGCTGATGAGCAAAATTTCTGAAGCTTATGAGGCTTATGATGAGGCA 558
DB 305 TCTTATTTCAAGCTGATGAGCAAAATTTCTGAAGCTTATGAGGCTTATGATGAGGCA 364
QY 559 GCGCAAGATTGAGACCATCAAAATTTCTGAAGCTTATGAGGCTTATGAGGCA 593
DB 365 GCGCAAAATTGAGACCATCAAAATTTCTGAAGCTTATGAGGCTTATGAGGCA 399

RESULT 2
AAF85192
ID AAF85192 standard; cDNA; 1250 BP.
XX AAF85192;
AC AAF85192;
DT 09-JUL-2001 (first entry)
DE Nucleotide sequence of a maize ZmMAD3 protein.
XX
XX
XX MA03; ZmMAD3; flower development; flower structure; seed development;
KM fruit development; transgenic plant; ss.
OS
XX
XX Zea mays.
XX
XX
XX Key Location/Qualifiers
FT CDS 70..882
FT /*tag= a
FT /product= "ZmMAD3"

XX
PN WO200131017-A2.
XX
XX 03-MAY-2001.
XX
XX 25-OCT-2000; 2000WO-EP10484.
XX
XX 25-OCT-1999; 99EP-0120842.
XX
XX (SUSD-) SUEDEWESTDEUTSCHE SAATZUCHT.
XX
XX Dresselhaus T, Heuer S, Loez H;
XX
XX WPI; 2001-316335/33.
DR P-PSDB; AAB68357.
XX

PT New polynucleotide encoding ZmMAD3 protein, for use in cloning and
PT expression in plant a nucleic acid sequence encoding protein
PT influencing flower structure, function and/or its seed and/or fruit
PT development
PS
PS Claim 1; Page 67; 71pp; English.

CC The present sequence encodes a maize MAD3 protein, designated ZmMAD3.
CC The ZmMAD3 protein is essential for flower development and is active
CC in flowers, in particular, in immature flowers and female flowers,
CC but also in the mature embryo sac of maize. The ZmMAD3 protein is also
CC active in nodes and adjacent cell layers. ZmMAD3 polynucleotides and
CC polypeptides are useful in influencing flower structure, function and
CC seed or fruit development in transgenic plants.

Sequence 1250 BP; 361 A; 295 C; 352 G; 242 T; 0 other;

Query Match 51.0%; Score 302.6; DB 22; Length 1250;
Best Local Similarity 93.7%; Pred. No. 7.7e-76;
Matches 314; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 259 GGATATGCGTCCGCGGCAAGCTGAGTGAAGCGATAGAAACAAGATAAATCGCAGGT 318
DB 66 GAAGATGGGGCCGCGCAAGCTGAGTGAAGCGATAGAAACAAGATAAATCGCAGGT 125
QY 319 GACCTTCTCAAGCGCGCAAGCGGCTCTGAAGAGCGCGAGATCTCGCTCTTG 378
DB 126 GACCTTCTCAAGCGCGCAAGCGGCTCTGAAGAGCGCGAGATCTCGCTCTTG 185
QY 379 TGACCGGAGGTCGCGCTGATGCTTTCTCCCAAGGCAAGCTCTATGATGAGCCAC 438
DB 186 CGAGCGCGAGGTCGCGCTGATGCTTTCTCCCAAGGCAAGCTCTATGATGAGCCAC 245
QY 439 CGACTTCAGCATGAGCAAAATTTCTGAAGCTTATGAGGCTTATGATGAGGCA 498
DB 246 CGACTTCAGCATGAGCAAAATTTCTGAAGCTTATGAGGCTTATGATGAGGCA 305
QY 499 TCTTATTTCAAGCTGATGAGCAAAATTTCTGAAGCTTATGAGGCTTATGAGGCA 558
DB 306 TCTTATTTCAAGCTGATGAGCAAAATTTCTGAAGCTTATGAGGCTTATGAGGCA 365
QY 559 GCGCAAGATTGAGACCATCAAAATTTCTGAAGCTTATGAGGCTTATGAGGCA 593
DB 366 GCGCAAAATTGAGACCATCAAAATTTCTGAAGCTTATGAGGCTTATGAGGCA 400

RESULT 3
AAT99437
ID AAT99437 standard; cDNA; 1342 BP.
XX AAT99437;
AC AAT99437;
DT 11-MAY-1998 (first entry)
DE Maize floral meristem identity gene APETALA (AP1 or ZAP-1) cDNA.
XX
XX
XX Floral meristem identity gene; APETALA1, AP1 gene; maize; ZAP-1;

flower development; transgenic plant; angiosperm; ss.

Zea mays.

Key Location/Qualifiers
149..970
/*tag= a

W09727287-A1.

31-JUL-1997.

26-JAN-1996; 96WO-US01041.

26-JAN-1996; 96WO-US01041.

(REGC) UNIV CALIFORNIA.

Yanofsky MF;

WPI, 1997-393675/36.
P-PSDB; AAW23814.

CAULIFLOWER floral meristem identity genes and related proteins -
used to develop products for converting shoot meristem to floral
meristem and promoting early flowering in an angiosperm

Example 1; Fig 4A-B; 132pp; English.

This sequence comprises maize ZAP-1 cDNA, which encodes a floral
meristem identity gene product (see AAW23814) that is involved in the
conversion of shoot meristem to floral meristem. The clone was
isolated from a Zea mays ear cDNA library using Arabidopsis API
cDNA (see AAT76885) as probe. Sequence homology indicates that
ZAP-1 is the maize orthologue of Arabidopsis APETALA-1 (API).
Mutation of an API gene results in replacement of a few basal
flowers by inflorescence shoots that are not subtended by flowers.
When API is ecotopically expressed in shoot meristem, the shoot
meristem is converted to floral meristem and early flowering can
occur. The invention relates to floral meristem identity genes
CC API, LFY and especially CAL (see AAT76885-97 and AAT99437) and their
use in converting shoot meristem to floral meristem and in
CC promoting early flowering in transgenic plants, especially
angiosperms such as cereal plants, leguminous plants, oilseed
plants, trees, fruit-bearing plants and ornamental flowers.

Sequence 1342 BP; 347 A; 373 C; 358 G; 264 T; 0 other;

Query Match 50.7%; Score 300.4; DB 18; Length 1342;
Best Local Similarity 92.4%; Pred. No. 3.3e-75;
Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

252 GAATCAGATATGGGTGCGGCGGCAAGTGCAGCTGAAGCGATGAGAAACAAGATAATC 311
138 GCAACAAGGCGATGGGGCGGCGCAAGTACAGCTGAAGCGATGAGAAACAAGATAATC 197
312 GCGAGGTGACCTTTCTCAAGCGCGCGCAAGCGGCTCTGAAAGAGCGCACGAGATCTCG 371
198 GCGAGGTGACCTTTCTCAAGCGCGCGCAAGCGGCTCTGAAAGAGCGCACGAGATCTCG 257
372 TCTCTGTGACGCGGAGGTGCGCGTATGCTTCTCCCGCAAGGCAAGCTTATGAGT 431
258 TCTCTGTGACGCGGAGGTGCGCGTATGCTTCTCTCCCGCAAGGCAAGCTTATGAGT 317
432 AGCCACCGACTCCAGCATGACAAATTTCTTGAAGCTATGAGCGCTACTTATGCTG 491
318 AGCCACCGACTCCAGCATGACAAATTTCTTGAAGCTATGAGCGCTACTTATGCTG 377
492 AAAAGCTCTTATTTAGCTGAATCTGAAAGTGAAGGAAATTTGTCGCAGATACAGGA 551
378 AAAAGCTCTTATTTAGCTGAATCTGAAAGTGAAGGAAATTTGTCGCAGATACAGGA 437
552 AACTTAAGCGAAGATTGAGACATACAAAATGTCAACG 593

438 AACTTAAGCGAAGATTGAGACATACAAAATGTCAACG 479

RESULT 4
AAV58307 standard; DNA; 1345 BP.

AAV58307 standard; DNA; 1345 BP.

AAV58307;

19-NOV-1998 (first entry)

Zea mays API gene.

CAULIFLOWER gene; CAL gene; shoot meristem conversion; floral meristem;
early flowering promotion; angiosperm; API gene; ZAP1; ds.

Zea mays.

Key Location/Qualifiers
149..970
/*tag= a

US5811536-A.

22-SEP-1998.

26-JAN-1996; 96US-0592214.

26-JAN-1996; 96US-0592214.

26-JAN-1996; 96US-0592214.

(REGC) UNIV CALIFORNIA.

Yanofsky MF;

WPI, 1998-530945/45.
P-PSDB; AAW69328.

Cloned CAULIFLOWER genes - and vectors for converting shoot
meristems to floral meristems

Example 1; Fig 4; 93pp; English.

This sequence encodes the Zea mays API protein (ZAP1). This sequence
was used to isolate DNA encoding the Arabidopsis thaliana CAULIFLOWER
(CAL) protein of the invention. An expression vector containing the CAL
DNA sequence can be used to convert shoot meristems to floral meristems,
especially to promote early flowering in angiosperms.

Sequence 1345 BP; 349 A; 373 C; 358 G; 265 T; 0 other;

Query Match 50.7%; Score 300.4; DB 19; Length 1345;
Best Local Similarity 92.4%; Pred. No. 3.3e-75;
Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

252 GAATCAGATATGGGTGCGGCGGCAAGTGCAGCTGAAGCGATGAGAAACAAGATAATC 311
138 GCAACAAGGCGATGGGGCGGCGCAAGTACAGCTGAAGCGATGAGAAACAAGATAATC 197
312 GCGAGGTGACCTTTCTCAAGCGCGCGCAAGCGGCTCTGAAAGAGCGCACGAGATCTCG 371
198 GCGAGGTGACCTTTCTCAAGCGCGCGCAAGCGGCTCTGAAAGAGCGCACGAGATCTCG 257
372 TCTCTGTGACGCGGAGGTGCGCGTATGCTTCTTCTCCCGCAAGGCAAGCTTATGAGT 431
258 TCTCTGTGACGCGGAGGTGCGCGTATGCTTCTTCTCCCGCAAGGCAAGCTTATGAGT 317
432 AGCCACCGACTCCAGCATGACAAATTTCTTGAAGCTATGAGCGCTACTTATGCTG 491
318 AGCCACCGACTCCAGCATGACAAATTTCTTGAAGCTATGAGCGCTACTTATGCTG 377
492 AAAAGCTCTTATTTAGCTGAATCTGAAAGTGAAGGAAATTTGTCGCAGATACAGGA 551

DB 378 AAAAGGCTTTATTTTCAGCTGAATCTGAAAGTGAGGAAAATTGGTCCACGAATACAGA 437
 QY 552 AACTTAAGCGGAAGATTGAGACCATACAAAATGTGCACAGC 593
 DB 438 AACTGAAGGCCAAATTAAGACCATACAAAATGTGCACAGC 479

RESULT 5
 AAT86631
 ID AAT86631 standard; DNA; 1345 BP.

AC AAT86631;

DT 18-JUN-1998 (first entry)

DE APETALA1 gene from Zea mays.

XX Transgenic plant; ectopically expressed; meristem gene; APETALA1;
 KM API; CAULIFLOWER; CAL; LEAFY; LFY; reproductive development;
 KW angiosperm; ds.

XX Zea mays.

XX Key Location/Qualifiers
 FT CDS 149..970
 FT /*tag= a
 FT /product= API_gene_product

PN W09746077-A1.

XX 11-DEC-1997.

XX 05-JUN-1996; 96WO-US09429.

XX 05-JUN-1996; 96WO-US09429.

XX (REGC) UNIV CALIFORNIA.

XX Weigel D, Yanofsky MF;

XX MPI: 1998-041769/04.

XX P-PSDB; AAW43112.

XX Transgenic plant comprising an ectopically expressed floral meristem
 PT gene - for promoting early reproductive development and controlling
 PT the time of seed-derived crop harvest(s) in e.g. grapes, beans,
 PT corn, wheat, etc

XX Example 5; Pages 125-127; 158pp; English.

XX The present sequence encodes a floral meristem identity gene product,
 CC APETALA1 (API), from Zea mays. The invention relates to a non-naturally
 CC occurring seed plant comprising a first ectopically expressible nucleic
 CC acid encoding a first floral meristem identity gene product, provided
 CC that the first nucleic acid is not ectopically expressed due to a
 CC mutation in an endogenous TERMINAL FLOWER gene. The invention describes
 CC a method of converting shoot meristem to floral meristem, especially in
 CC order to promote early reproductive development, in an angiosperm, which
 CC comprises introducing a first ectopically expressible nucleic acid
 CC molecule encoding a first floral meristem identity gene product into the
 CC angiosperm. Ectopic expression of the floral meristem gene product in
 CC the shoot meristem tissue of the transgenic plant, allows selection of
 CC the line of seed development in the plant which can be useful for
 CC manipulating the time of crop harvest in seed-derived crops such as
 CC grapes, beans, corn, wheat, rice, hop, etc., or to hasten the breeding
 CC of e.g. tree species, for insect or disease resistance.

XX Sequence 1345 BP; 349 A; 373 C; 358 G; 265 T; 0 other;

XX Query Match 50.7%; Score 300.4; DB 19; Length 1345;

XX Best Local Similarity 92.4%; Pred. No. 3.3e-75;

XX Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 252 GAAATCAGAGATATGGGTCCCGGCAAGTGCAGCTTGAGCCGATAGACAAAGATTAATC 311
 DB 138 GCAACAGAGCGATGGGCGCGGCAAGGTACAGCTGAAGCGGTAGACAAAGATTAAC 197
 QY 312 GGCAGGTGACCTTCTTCCAAAGCGCCGCAACGGCTCTTGAAGAGCGGCACGATCTCG 371
 DB 198 GGCAGGTGACCTTCTTCCAAAGCGCCGCAACGGCTCTTGAAGAGCGGCACGATCTCG 257
 QY 372 TCCTCTGTGACGCGGAGGTGCGCGGTATCTTCTCCCGCAAGGACCTTAATGAGT 431
 DB 258 TCCTCTGTGATGCGGAGGTGCGCGGTATCTTCTCCCGCAAGGACCTTATGAGT 317
 QY 432 ACGCACCGAGCTCCGACATGACCAAAATTTCTTGAAGCGGTATGAGCTTATGCTG 491
 DB 318 ACGCACCGAGCTCCGACATGACCAAAATTTCTTGAAGCGGTATGAGCTTATGCTG 377
 QY 492 AAAAGGCTTTATTTTCAGCTGAATCTGAAAGTGAGGAAATTTGGTCCACGAATACAGA 551
 DB 378 AAAAGGCTTTATTTTCAGCTGAATCTGAAAGTGAGGAAATTTGGTCCACGAATACAGA 437
 QY 552 AACTTAAGCGGAAGATTGAGACCATACAAAATGTGCACAGC 593
 DB 438 AACTGAAGGCCAAATTAAGACCATACAAAATGTGCACAGC 479

RESULT 6
 AAV02763

ID AAV02763 standard; cDNA; 1345 BP.

XX AAV02763;

XX 08-JUN-1998 (first entry)

XX Maize floral meristem identity gene APETALA1 (ZAPI) cDNA.

XX Floral meristem identity gene; APETALA1; API; ZAPI;

XX transgenic plant; angiosperm; seed development; maize; ds.

XX Zea mays.

XX Key Location/Qualifiers
 FT CDS 149..970
 FT /*tag= a

PN W09746078-A1.

XX 11-DEC-1997.

XX 05-JUN-1996; 96WO-US09453.

XX 05-JUN-1996; 96WO-US09453.

XX (REGC) UNIV CALIFORNIA.

XX Yanofsky MF;

XX MPI: 1998-041770/04.

XX P-PSDB; AAW39134.

XX Nucleic acids encoding API floral meristem identity gene product
 PT from cauliflower and maize - useful for promoting early reproductive
 PT development and controlling the time of seed-derived crop harvest in
 PT e.g. grapes, beans, corn, wheat, etc

XX Claim 2; Page 125-127; 156pp; English.

XX This sequence comprises maize APETALA (ZAPI) cDNA, which encodes
 CC a floral meristem identity gene product (see AAW39134) that is
 CC involved in the conversion of shoot meristem to floral meristem.
 CC It was isolated from an immature ear cDNA library using
 CC Arabidopsis API cDNA (see AAV02760) as probe, and is suggested to be
 CC the maize orthologue of API. Mutation of the API gene results in
 CC replacement of basal flowers by inflorescence shoots that are not

CC subbanded by flowers. The invention relates to an expression
 CC vector comprising a nucleic acid sequence encoding a floral
 CC meristem gene product operably linked to a heterologous regulatory
 CC element (see AAV02770-75). The floral meristem gene product is
 CC selected from API, LFY (LEAFY) and CAL (CAULIFLOWER) (see AAV02760-67).
 CC The expression vector is used to convert shoot meristem tissue to
 CC floral meristem tissue in transgenic plants, especially angiosperms
 CC or gymnosperms, thereby promoting early reproductive development in
 CC these plants. This can be used to manipulate the time of crop
 CC harvest and to hasten breeding time.

CC Sequence 1345 BP; 349 A; 373 C; 358 G; 265 T; 0 other;

Query Match 50.7%; Score 300.4; DB 19; Length 1345;
 Best Local Similarity 92.4%; Pred. No. 3.3e-75;
 Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

252 GAATTCAGATATGGTGGCGGCAAGTGCAGTGAAGCGATAGAGAACAAATTAATC 311
 138 GCACACAGCGCATGGGCGCGGCAAGTGCAGTGAAGCGATAGAGAACAAATTAATC 197
 312 GCGAGTGAACCTTCTCCAAAGCGCGCAAGCGGCTCTGAAGAGCGCAGATCTCCG 371
 198 GCGAGTGAACCTTCTCCAAAGCGCGCAAGCGGCTCTGAAGAGCGCAGATCTCCG 257
 372 TCTCTGTCAGCGGAGGTCGCGGTCATGCTCTTCCCGCAAGGCGCATCTATGAGT 431
 258 TCTCTGTCAGCGGAGGTCGCGGTCATGCTCTTCCCGCAAGGCGCATCTATGAGT 317
 432 ACGCCACCGACTCCAGCATGACAAATTTCTGAACGTTATGAGCGCTATCTATGCTG 491
 318 ACGCCACCGACTCCAGCATGACAAATTTCTGAACGTTATGAGCGCTATCTATGCTG 377
 492 AAAAGGCTTTATTTAGCTGAATCTGAAGAGGAGGAATTTGCTCCAGATACAGA 551
 378 AAAAGGCTTTATTTAGCTGAATCTGAAGAGGAGGAATTTGCTCCAGATACAGA 437
 552 AACTTAAGCGGAAGATTGAGACCATACAAATATGTCAACAGC 593
 438 AACTGAAGGCCAAATTTGAGACCATACAAATATGTCAACAGC 479

RESULT 7
 AAV06021

ID AAV06021 standard; cDNA; 1345 BP.

AC AAV06021;

08-JUN-1998 (first entry)

DE Maize floral meristem identity gene APTALAI orthologue cDNA.

KW Floral meristem identity gene; APTALAI; API; ZAPI; maize;

KW transgenic plant; angiosperm; seed development; ds.

OS Zea mays.

Key Location/Qualifiers
 CDS 149..970
 /*tag= a

PN MO9746079-A1.

PD 11-DEC-1997.

PF 04-JUN-1997; 97MO-US09682.

PR 05-JUN-1996; 96US-0659188.

XX (REGC) UNIV CALIFORNIA.

PI Yanofsky MF;

XX

DR WPI; 1998-041771/04.
 P-PDB; AAW43329.

PT Use of floral meristem identity genes to convert shoot meristem to
 PT floral meristem - for promoting early reproductive development in
 PT the plants and control timing of seed-derived crop harvest (s) in
 PT e.g. grapes, beans, corn and wheat

PS Claim 6; Page 110-112; 147pp; English.

CC This sequence comprises maize ZAPI cDNA, which encodes a floral
 CC meristem identity gene product (see AAW43329) that is involved in the
 CC conversion of shoot meristem to floral meristem. It was isolated
 CC from an immature ear cDNA library using Arabidopsis API cDNA (see
 CC AAV06018) as probe, and is suggested to be the maize orthologue of API.
 CC Mutation of the API gene results in replacement of basal flowers by
 CC inflorescence shoots that are not subtended by flowers. The
 CC invention relates to a recombinant nucleic acid molecule that
 CC comprises an inducible regulatory element (see AAV06025-28) operably
 CC linked to a nucleic acid molecule (see AAV06018-24) encoding a floral
 CC meristem identity gene product (see AAW43326-32), especially API,
 CC CAULIFLOWER (CAL) or LEAFY (LFY). The nucleic acids are used to
 CC convert shoot meristem tissue into floral meristem tissue in
 CC transgenic plants, thereby promoting early reproductive development
 CC in these plants. This can be useful for manipulating the time of
 CC crop harvest in seed-derived crops and to hasten breeding time.

Sequence 1345 BP; 349 A; 373 C; 358 G; 265 T; 0 other;

Query Match 50.7%; Score 300.4; DB 19; Length 1345;
 Best Local Similarity 92.4%; Pred. No. 3.3e-75;
 Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

252 GAATTCAGATATGGTGGCGGCAAGTGCAGTGAAGCGATAGAGAACAAATTAATC 311
 138 GCACACAGCGCATGGGCGCGGCAAGTGCAGTGAAGCGATAGAGAACAAATTAATC 197
 312 GCGAGTGAACCTTCTCCAAAGCGCGCAAGCGGCTCTGAAGAGCGCAGATCTCCG 371
 198 GCGAGTGAACCTTCTCCAAAGCGCGCAAGCGGCTCTGAAGAGCGCAGATCTCCG 257
 372 TCTCTGTCAGCGGAGGTCGCGGTCATGCTCTTCCCGCAAGGCGCATCTATGAGT 431
 258 TCTCTGTCAGCGGAGGTCGCGGTCATGCTCTTCCCGCAAGGCGCATCTATGAGT 317
 432 ACGCCACCGACTCCAGCATGACAAATTTCTGAACGTTATGAGCGCTATCTATGCTG 491
 318 ACGCCACCGACTCCAGCATGACAAATTTCTGAACGTTATGAGCGCTATCTATGCTG 377
 492 AAAAGGCTTTATTTAGCTGAATCTGAAGAGGAGGAATTTGCTCCAGATACAGA 551
 378 AAAAGGCTTTATTTAGCTGAATCTGAAGAGGAGGAATTTGCTCCAGATACAGA 437
 552 AACTTAAGCGGAAGATTGAGACCATACAAATATGTCAACAGC 593
 438 AACTGAAGGCCAAATTTGAGACCATACAAATATGTCAACAGC 479

RESULT 8
 AAC61410

ID AAC61410 standard; cDNA; 1345 BP.

AC AAC61410;

19-FEB-2001 (first entry)

DE cDNA encoding a APTALAI (API) polypeptide.

KW APTALAI; API; floral meristem identity gene; CAULIFLOWER; CAL; LEAFY;

KW LFY; floral meristem; early flowering; ds.

OS Zea mays.

XX

Key Location/Qualifiers
CDS 149..970
/*tag= a
/product= "APETALAI"

US6127123-A.
03-OCT-2000.
09-SEP-1998; 98US-0149976.
26-JAN-1996; 96US-0592214.
(REGC) UNIV CALIFORNIA.
Yanofsky MF;
WPI: 2000-618379/59.
P-PSDB; AAB19244.

Identifying a Brassica having a cauliflower phenotype involves detecting a polymorphism associated with cauliflower locus comprising a modified cauliflower allele that does not encode active cauliflower gene product -

Example 1; Fig 4A-B; 93pp; English.

The present sequence encodes an APETALAI (Api) polypeptide. The Api polypeptide is an ectopically expressible floral meristem identity gene product. The specification also describes CAULIFLOWER (CAL) and LEAFY (LFY) gene products. CAL is involved in the conversion of shoot meristem to floral meristem. CAL is highly conserved among different angiosperms. The CAL polynucleotides may be used to shoot meristem to floral meristem, and to promote early flowering in angiosperms.

Sequence 1345 BP; 349 A; 373 C; 358 G; 265 T; 0 other;

Query Match 50.7%; Score 300.4; DB 21; Length 1345;
Best Local Similarity 92.4%; Pred. No. 3.3e-75;
Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

252 GAAATCAGATATGGTGGCGGCAAGTGCAGCTGAGCGGATAGAAACAAGATTAATC 311
138 GCACACAGCGATGGGCGCGCAAGTACAGCTAAGCGGATAGAAACAAGATTAACC 197
312 GGCAGTACCTTCCAAAGCGCGCAAGGGCTCTGAGAGGCGCAAGATCTCCG 371
198 GGCAGTACCTTCTCAAGCGCGCAAGGGCTCTGAGAGGCGCAAGATCTCCG 257
372 TCCTCTGAGACGCGAGGTGCGCGTCAATGCTCTCCGCCCAAGGCAAGCTCTATGAGT 431
258 TCCTCTGAGATGCGAGGTGCGCGTCAATGCTCTCTCCGCCCAAGGCAAGCTCTATGAGT 317
432 ACGCCACCGAGTCCAGCATGACAAAAATTTCTGAAGCTTATGAGCGCTACTTATGCTG 491
318 ACGCCACCGAGTCCCGCATGACAAAAATTTCTGAAGCTTATGAGCGCTACTTATGCTG 377
492 AAAAGGCTCTTATTTCACTGATGTAATGTAAGAGGAAATTTGGTCCCAAGATACAGA 551
378 AAAAGGCTCTTATTTCACTGATGTAATGTAAGAGGAAATTTGGTCCCAAGATACAGA 437
552 AACTTAAGCGAAGATTGAGACCATACAAAATTTGTCACAAGC 593
438 AACTGAAGCCAAATTTGAGACCATACAAAATTTGTCACAAGC 479

RESULT 9
AAZ57057
ID AAZ57057 standard; DNA; 1345 BP.
XX AC AAZ57057;
XX DT 19-MAY-2000 (first entry/)

XX Zea mays ZAPI protein encoding DNA.
DE
XX Seed plant; floral meristem; mutation; TPL gene; CAL;
KW reproduction; plant breeding; Api protein; ds.
XX
XX Zea mays.
OS
XX US6025543-A.
XX
XX 15-FEB-2000.
XX
XX 05-JUN-1996; 96US-0655241.
XX
XX 05-JUN-1996; 96US-0655241.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Yanofsky MF;
XX
XX WPI: 2000-181843/16.
XX
XX P-PSDB; AAV67553.
XX
XX New transgenic seed plant exhibiting early reproductive development
PT comprises a CAULIFLOWER encoding nucleic acid and a non-mutant
PT endogenous TERMINAL FLOWER gene -
XX
XX
XX Example 5; Columns 59-64; 51pp; English.

The invention relates to a new non-naturally occurring seed plant that comprises a first ectopically expressible nucleic acid molecule encoding a floral meristem identity gene product, provided that the seed plant does not contain a mutation in an endogenous TERMINAL FLOWER (TFL) gene that results in ectopic expression of CAL. The non-naturally occurring seed plant exhibits early reproductive development. The method of promoting early reproductive development can make breeding of long generation seed plants such as trees practical. The method can be used to increase floral meristem identity gene product expression in different crop fields at different times, resulting in a staggered time of harvest for the different fields. The present sequence represents a Zea mays Api protein encoding DNA.

Sequence 1345 BP; 349 A; 373 C; 358 G; 265 T; 0 other;

Query Match 50.7%; Score 300.4; DB 21; Length 1345;
Best Local Similarity 92.4%; Pred. No. 3.3e-75;
Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

252 GAAATCAGATATGGTGGCGGCAAGTGCAGCTGAGCGGATAGAAACAAGATTAATC 311
138 GCACACAGCGATGGGCGCGCAAGTACAGCTAAGCGGATAGAAACAAGATTAACC 197
312 GGCAGTACCTTCTCAAGCGCGCAAGGGCTCTGAGAGGCGCAAGATCTCCG 371
198 GGCAGTACCTTCTCAAGCGCGCAAGGGCTCTGAGAGGCGCAAGATCTCCG 257
372 TCCTCTGAGACGCGAGGTGCGCGTCAATGCTCTCCGCCCAAGGCAAGCTCTATGAGT 431
258 TCCTCTGAGATGCGAGGTGCGCGTCAATGCTCTCTCCGCCCAAGGCAAGCTCTATGAGT 317
432 ACGCCACCGAGTCCAGCATGACAAAAATTTCTGAAGCTTATGAGCGCTACTTATGCTG 491
318 ACGCCACCGAGTCCCGCATGACAAAAATTTCTGAAGCTTATGAGCGCTACTTATGCTG 377
492 AAAAGGCTCTTATTTCACTGATGTAATGTAAGAGGAAATTTGGTCCCAAGATACAGA 551
378 AAAAGGCTCTTATTTCACTGATGTAATGTAAGAGGAAATTTGGTCCCAAGATACAGA 437
552 AACTTAAGCGAAGATTGAGACCATACAAAATTTGTCACAAGC 593
438 AACTGAAGCCAAATTTGAGACCATACAAAATTTGTCACAAGC 479

RESULT 10

AAZ92144
ID AAZ92144 standard; cDNA; 1345 BP.

AAZ92144;

19-MAY-2000 (first entry)

Corn APETALA1 (Api) nucleotide sequence.

APETALA1; Api; floral meristem identity; early reproductive development; transgenic plant; selective breeding programme; disease resistance; corn; ds.

Zea mays.

US6025483-A.

15-FEB-2000.

05-JUN-1996; 96US-0655227.

05-JUN-1996; 96US-0655227.

(REGC) UNIV CALIFORNIA.

Yanofsky MF;

WPI; 2000-181839/16.

P-PSDB; AAY78883.

Purified nucleic acids encoding APETALA 1 (Api) proteins, promote early reproductive development in seed plants, useful for accelerating selective breeding programmes

Claim 1; Column 59-62; 50pp; English.

This sequence represents the APETALA1 (Api) gene sequence from corn. Api is a floral meristem identity product, that promotes conversion of shoot meristem to floral meristem in an angiosperm. Vectors containing the Api gene can be used to create transgenic plants. Api nucleotide sequences can be used to promote early reproductive development in seed plants which is useful for accelerating selective breeding programmes that require several rounds of crossing to produce plants with disease and insect resistance. The nucleotide sequences are particularly useful for promoting early reproductive development in long generation seed plants such as trees.

Sequence 1345 BP; 349 A; 373 C; 358 G; 265 T; 0 other;

Query Match 50.7%; Score 300.4; DB 21; Length 1345;
Best Local Similarity 92.4%; Pred. No. 3.3e-75;
Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

252 GAAATAGATATGGTTCGCGCAGGTGAGTGAAGCGATAGAGCAAGATTAATC 311
138 GCAACAAGCGATGGGGCCGCGCAAGTACAGTGAAGCGATAGAGCAAGATTAATC 197
312 GCGAGTGAACCTTCTCCAAAGCGCGCAAGCGGCTCTGAGAGAGCGCAAGATTCGG 371
198 GCGAGTGAACCTTCTCCAAAGCGCGCGAGCGCTGCTCAAGAGAGCGCAAGATTCGG 257
372 TCCCTGTACGCGGAGGTCCGTCATGCTCTTCCCGCAAGCGCAAGCTTATAGAT 431
258 TCCCTGTACGCGGAGGTCCGTCATGCTCTTCCCGCAAGCGCAAGCTTATAGAT 317
432 ACGCCACGACTCCAGATGAGCAAAATCTTGAAGTTATGAGCGCTACTTATGCTG 491
318 ACGCCACGACTCCAGATGAGCAAAATCTTGAAGTTATGAGCGCTACTTATGCTG 377
492 AAAAGGCTCTTATTTAGCTGAATCTGAAGTGAAGGAAATGGTCCAGATTAACGA 551
378 AAAAGGCTCTTATTTAGCTGAATCTGAAGTGAAGGAAATGGTCCAGATTAACGA 437

552 AACTTAAGCGAAGTTGAGACCATACAAAATGTCAACAGC 593
438 AACTGAAGCCCAAAATTGAGACCATACAAAATGTCAACAGC 479

RESULT 11

AAZ92144
ID AAF75749 standard; DNA; 1289 BP.

AAZ92144;

14-MAY-2001 (first entry)

Rice MADS box gene.

Rice; MADS box; plant branching regulation; agriculture; ds.

Oryza sativa.

WO200114559-A1.

01-MAR-2001.

18-AUG-2000; 2000WO-JP05537.

19-AUG-1999; 99JP-0232318.

(TSUB) KUMIAT CHEM IND CO LTD.

(KOJI) KOJIMA M.

Kojima M, Sasaki T, Nozue M, Shioiri H;
WPI; 2001-191647/19.
P-PSDB; AAB73250.

Rice MADS box gene for regulating plant branching to provide ornamental or agricultural plants with value-added properties or increase in yield

Claim 3; Page 19-20; 43pp; Japanese.

The present sequence is a gene which contains the rice MADS box gene. This sequence can be used for regulating plant branching to provide ornamental or agricultural plants. In addition, plants with value-added properties or an increased yield can be produced using the present sequence.

Sequence 1289 BP; 354 A; 316 C; 337 G; 282 T; 0 other;

Query Match 47.8%; Score 283.2; DB 22; Length 1289;
Best Local Similarity 89.0%; Pred. No. 2.5e-70;
Matches 306; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

250 GGAATAGATATGGTTCGCGCAGGTGAGTGAAGCGATAGAGCAAGATTAATC 309
112 GCGACGCGGAGGATGGGGCCGCGCAAGTACAGTGAAGCGATAGAGCAAGATTAATC 171
310 TCGGAGGTGACCTTCTCCAAAGCGCGCAAGCGGCTCTGAGAGAGCGCAAGATTCG 369
172 CAGGAGGTGACCTTCTCCAAAGCGCGCAAGCGGCTCTGAGAGAGCGCAAGATTCG 231
370 GGTCTGTACGCGGAGGTCCGTCATGCTCTTCCCGCAAGCGCAAGCTTATAGAT 429
232 GGTCTGTACGCGGAGGTCCGTCATGCTCTTCCCGCAAGCGCGCAAGCTTATAGAT 291
430 GTACCCACCGACTCCAGATGAGCAAAATCTTGAAGTTATGAGCGCTACTTATGCTG 489
292 GTACCCACCGACTCCAGATGAGCAAAATCTTGAAGTTATGAGCGCTACTTATGCTG 351
490 TGAAGGCTCTTATTTAGCTGAATCTGAAGTGAAGGAAATGGTCCAGATTAACGA 549
352 TGAAGGCTCTTATTTAGCTGAATCTGAAGTGAAGGAAATGGTCCAGATTAACGA 411


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PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0148368.
PR 17-AUG-1999; 99US-0148175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 18-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match 38.7%; Score 229.4; DB 21; Length 466;
 Best Local Similarity 91.3%; Pred. No. 3.2e-55;
 Matches 242; Conservative 1; Mismatches 22; Indels 0; Gaps 0;

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OY 252 GAAATAGATATAGGTCCGGCAAGTGCAGCTGATAGGATAGGAACAAGATTAATC 311
DB 202 GCAACAAGCGATGGGCGCGCAAGGTACAGCTGAAGCGGATAGGAACAAGATTAACC 261
OY 312 GCGAGGTGACCTTCTCCAAAGCGCGCAAGCGGCTCCTGGAAGAGCGCAAGATCTCG 371

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DB 262 GCGAGTGACCTTCTCCAAAGCGCGCAAGCGCTGTCTCAAGAGCGCACAGATCTCCG 322
OY 372 TCCTCTGAGCGGAGGTGGCGTCATCGCTTCTCCGCCCAAGGCAAGCTTATGAGT 431
DB 322 TCCTCTGAGTCCGAGGTGGCGTCATCGCTTCTCCGCCCAAGGCAAGCTTATGAGT 381
OY 432 ACGCACCAGACTCCAGATGACCAAAATTTCTTGAAGCTTATGAGCGCTACTCTTATGCTG 491
DB 382 ACGCACCAGACTCCCGATGACCAAAATTTCTTGAAGCTTATGAGCGATATTCCTATGCTG 441
OY 492 AAAAGCTCTTATTTCAAGCTGATC 516
DB 442 AAAAGCTCTTATTTCAAGCTGATC 466

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RESULT 13

AAT34430
 ID AAT34430 standard; cDNA; 1032 BP.

AC AAT34430;

DT 01-OCT-1996 (first entry)

DE Eucalyptus SOE2S cDNA.

KW Eucalyptus; reproductive gene; SOE2S; Arabidopsis; agamous gene;

KW Antirrhinum; plena gene; sterility; fertility; forest tree;

KW transgenic plant; flower development; antisense; ribozyme; ss.

OS Eucalyptus globulus.

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Query Match 32.9%; Score 195; DB 17; Length 1032;
 Best Local Similarity 71.8%; Pred. No. 2.6e-45;

Sequence 1032 BP; 299 A; 231 C; 263 G; 239 T; 0 other;
 CDNA clones SOE1 (AAT34429), SOE2S (AAT34430) and SOE2L (AAT34431) were
 identified by homology to the MADS box of the Arabidopsis apical
 1 (AP1) and Antirrhinum squamosa (SQUA) flower development genes.
 They were obtained by PCR amplification of E. globulus DNA using
 primers based on the MADS box of the Arabidopsis and Antirrhinum
 genes, followed by screening of a E. globulus young flower bud
 library. The SOE2S cDNA codes for protein SOE2-S (AA99635).
 CC Antisense or ribozyme constructs of SOE, or of FLE2 and SOE genes
 (see also AAT34426, AAT34428 and AAT34432), may be used to produce
 sterile transgenic Eucalyptus trees by minimising inflorescence.

Matches	255; Conservative	0; Mismatches	100; Indels	0; Gaps	0
QY	238	GACAGCTGATGCGGAATCAGAGATATGSGTCGCGGCAGAGTGACAGCTGAAGCGATAGA	297		
Db	159	GAGGAGAGAGAGTGTAGAGAGAAAAATGGGGAGGGGGAGGGGTGCAGCTGAAAGAGATAGA	218		
QY	298	GAAACAAGTAAATGGCGAGGTGACCTTCTCCAAAGCGCCGCAACGGGCTCTCTGAAGAAGGC	357		
Db	219	GAAACAAGTAAACAGGCAAGATGACGTTCTTCGAAGCGGAATGCGGGCTGCTGAAGAAGGC	278		
QY	358	GCACGAGATCTCCGTCCTCTGTGACGCGGAGGTGCGCGCTCATCGTCTTCTCCCAAGG	417		
Db	279	CCAGGAGATCTCCGTCCTCTGTGGAAGCGGACGTCGCTCATCGTCTTCTCCACCAAGGG	338		
QY	418	CAAGCTCATGAGTACGCCACCGACTCCAGCATGACAAAAATTTCTTGAACGTTATGAGCG	477		
Db	339	CAAGCTCTTCGAGTACGCCACCGACTGTCATGGAGAGAGATCTTCGACGCTTATGATAG	398		
QY	478	CTACTCTTATGCTGAAGAAGCCTCTTATTTCACTGAATGTGAAGTGAAGGAAATTTGCTG	537		
	399	ATATTCATATGAGAGAAACGAGGTTCTCACAAACAATGCCGAACCAATGGGAACCTGGAC	458		
QY	538	CCACGATATACAGGAACCTTAAAGCGCAAGTTAGACCAATACAAAAATGTCCACAG	592		
Db	459	TTTGGAAACATGCAAAATCTCAGGCCAGATGAGATCTTCGCAAAAAATCAAAAG	513		

RESULT 14
AAT34431
ID AAT34431 standard; cDNA; 1070 BP.

DT 01-OCT-1996 (first entry)

DE Eucalyptus SQE2L cDNA

Eucalyptus; reproduct:

KW transgenic plant; flower development; antisense; ribozyme; ss.

OS Eucalyptus globulus.

FH	Key	Location/Qualifiers
1		

F^T / *tag= a

AU9539013-A

PD 30-MAY-1996

PF 22-NOV-1995; 95AU-0039013.

PR 22-NOV-1994; 94AU-0009589.

PA (CSIR) COMMONWEALTH SCI & IND RES ORG

PI Dennis ES, Harcourt RL, Kyozeuka J, Llewellyn D,

XX XX

DR P-PSDB; AAR99636.

PT Eucalyptus reproductive genes - useful for prodn. of sterile

PT re-forestation projects

PS Claim 8; Page 36-37; 60pp; English

CC cDNA clones SQE1 (AAT34429), SQE2S (AAT34430) and SQE2L (AAT34431) were
CC identified by homology to the MADS box of the *Arabidopsis* *apetala*
CC 1 (API) and *Antirrhinum* *squamosa* (SQUA) flower development genes.

CC They were obt'd. by PCR amplification of *E. glaberrimus* DNA using
CC primers based on the MADS box of the *Arabidopsis* and *Antirrhinum*
CC genes, followed by screening of a *E. glaberrimus* young flower bud
CC library. The SQE2L cDNA codes for a protein SQE2-L (AA099636).
CC *Antirrhinum* or fibrozyne constructs of SQE, or of *FLZ* and SQE genes
CC (see also A0134426, A0134428 and A0134432), may be used to produce
CC sterile transgenic *Eucalyptus* trees by maintaining inflorescence.
XX
XX Sequence 1070 BP; 308 A; 240 C; 270 G; 252 T; 0 other;
X0

Query Match	32.9%;	Score 195;	DB 17;	Length 1070;
Best Local Similarity	71.8%;	Pred. No. 2.7e-45;		
Matches 255; Conservative	0;	Mismatches 100;	Indels 0;	Gaps 0;

Qy	238	GACAGTATATGATCGCAAAATCAGAGATATGGATTCGGCGCAAGGTGACGTGTAAGCGGATAGA	297
Db	159	GAGCGAGAGAGCTGATGAGAGAAATATGGAGAGGGGGAGGGGTGACGCTGTAAGAGGATAGA	218
Qy	298	GAAACAAGATAAATCGCGCAGGTGACCTTCTCCAAACGCGCCCAACGGGCTCTCTGAAAGAGGC	357
Db	219	GAAACAAGATAAACAAGCAAGTATGACCTTTCGAACGCGAGATCGGGCTGCTGAAAGAGGC	278
Qy	358	GCAAGAGATCTCCGCTCTCTGTGACGCGAGAGTGCAGCATCGTCTTCTCCCAAGG	417
Db	279	CAAGAGATCTCCGCTCTCTGTGACGCGAGAGTGCAGCATCGTCTTCTTCTCAACAAAGG	338

Db 339 CAAGCTCTTCGAGTAGCGCACCGACTGTTCATGAGAGAGATCCTCGAGCGTTATGAGAG 398

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RESULT 15

ID AAC44058 standard; DNA; 1305 BP.

AC AAC440582

DT 18-OCT-2000 (first entry)

DE Zea mays DNA fragment SEQ ID NO: 41467.

KW Hybridisation assay; genetic mapping; gene expression control;

KW pathway; promoter; termination sequence; corn; ss

Zea mays subsp. *mays*.

PN EP1033405-A2

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439

PR 25-FEB-1999; 99US-0121825.

PR 09-MAR-1999; 99US-0123548

PR 25-MAR-1999; 99US-0126264

PR 01-APR-1999; 99US-0127462.

PR 08-APR-1999; 99US-0128714

PR 19-APR-1999; 99US-0130077

PR 23-APR-1999; 99US-0130510.
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Query Match 31.9%; Score 189.4; DB 21; Length 1305;
 Best Local Similarity 72.8%; Pred. No. 1.1e-43;
 Matches 244; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 259 GGATATGGGTCCGGCGAAGTGCAGCTGAAGCGGATAGAGAACAAATATCGGAGGT 318
 DB 166 GGAGATGGGGCGGGCGCCGCTGCGCGGATCGAGAACAGATCAACCGCCAGGT 225
 QY 319 GACCTTCTCCAGCGCGCGAAGCGGCTCCTGAAGAGCGCACGAGATCTCCGCTCTG 378
 DB 226 GACCTTCTCCAGCGCGCGAAGCGGCTCCTGAAGAGCGCACGAGATCTCCGCTCTG 285
 QY 379 TGACCGGAGGTGCGCGTATGCTCTTCTCCCGAAGGCAAGCTCTATGATGCGCAC 438
 DB 286 CGACGCGAGGTGCGCGCTATGCTCTTCTCCAGTAAAGGAGCTCTACGAGTACTCTAG 345
 QY 439 CGACTCCAGCATGSAACAAATCTTGAAGTTATGAGCGCTACTTATGCTGAAGAGC 498
 DB 346 CATTTCACGATGGAAGGCAATCTTGAAGGTACCGCGTTACTATTGAAGAAAGGCGC 405
 QY 499 TCTTATTTGAGTGAATCTGAAAGTGAGGAAATTGTCGACGATACAGGAACTTAA 558
 DB 406 AGTACTTAACCAAGATTTGAAGACCGCAAAATTGGGAGATGATATGTCGGTTAAA 465
 QY 559 GCGGAGATTGAGACCATACAAAATGTCACAAGC 593
 DB 466 ATCCAAACTTGATGCACTTCAGAAAGTCAAAAGC 500

Search completed: June 29, 2003, 07:29:46
 Job time : 162 secs

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Page 7

Page 7

Page 7

Page 7

Page 7

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; Sequence 13, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Brassica oleracea var. botrytis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(453)
; OTHER INFORMATION: CAULIFLOWER
; US-09-853-450-13

Query Match          22.2%; Score 131.4; DB 9; Length 756;
Best Local Similarity 66.0%; Pred. No. 8e-32;
Matches 208; Conservative 0; Mismatches 101; Indels 6; Gaps 1;

QY 263 ATGGGTGCGCGCAAGTGCAGCTGAAGCGGATAGAGAACAGATTAATCGCAGGTGACC 322
DB 1 ATGGGAAGAGGATAGAGTTGAATAGAAAGAGATAGAGAACAGATCAACAGCAAGTACG 60
QY 323 TTCTCCAAAGCGCCGCAACGGGCTCTCTGAAGAGCGGACGAGATCTCCGTCCTGTAC 382
DB 61 TTTCGAAAGGCTAGAGACGGTTGTTGAAGAAAGCCATGAGATCTCATTTCTTTGTAT 120
QY 383 GCGGAGGTGCGCGTATCGTCTTCTCCCAAGGCAAGCTCTATGATAGCCACCGAC 442
DB 121 GCTGAGTTTCCCTTATGTTCTTCTCCATAGGGGAACTTTGAGATCTCGCTGAA 180
QY 443 TCCAGCATGACAAATTTCTTGAACGTTATGAGCGCTACTTATGCTGAAAAGGCTCTT 502
DB 181 TCTTGATGAGAGAGTACTAGAAAGTACGAGAGTACTCTTACGCCGAGAAACAGCTA 240
QY 503 ATTTCAGTGAATCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 556
DB 241 AAAGCTCCAGACTCTCAGCTCAATGCAACAAAGAACTGCTCAATGAAATATAGAGGCTT 300
QY 557 AAGGCAAGATTGAG 571
DB 301 AAGGCTAAGATTGAG 315

RESULT 13
US-09-853-450-27
; Sequence 27, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(747)
; OTHER INFORMATION: SEPALLATA1 (SEP1)
; US-09-853-450-27

Query Match          19.4%; Score 114.8; DB 9; Length 747;
Best Local Similarity 60.1%; Pred. No. 1.7e-26;
Matches 191; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 263 ATGGGTGCGCGCAAGTGCAGCTGAAGCGGATAGAGAACAGATTAATCGCAGGTGACC 322
DB 1 ATGGGAAGAGGATAGAGTTGAATAGAAAGAGATAGAGAACAGATCAACAGCAAGTACG 60
QY 323 TTCTCCAAAGCGCCGCAACGGGCTCTCTGAAGAGCGGACGAGATCTCCGTCCTGTAC 382
DB 61 TTTCGAAAGGCTAGAGACGGTTGTTGAAGAAAGCCATGAGATCTCATTTCTTTGTAT 120
QY 383 GCGGAGGTGCGCGTATCGTCTTCTCCCAAGGCAAGCTCTATGATAGCCACCGAC 442
DB 121 GCTGAGTTTCTCTCATCATCTTCTCCACCGTGAAGACTCTATGAGTTTGAAGCTCC 180
QY 443 TCCAGCATGACAAATTTCTTGAACGTTATGAGCGCTACTTATGCTGAAAAGGCTCTT 502
DB 181 TCAACATGCTCAAGACACTTATGATCGGTACAGAAATGACAGCTATGATCATGAAATC 240
QY 503 ATTTCAGTGAATCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 562
DB 241 AACAAACAACTGCGCAAGAACTTGAGAACAGCTACAGAAATCTGAAGCTTAAGGCT 300
QY 563 AAGATTGAGACCATACAA 580
DB 301 AGATATGAGAACTTCAA 318

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US-09-853-450-29
; Sequence 29, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(753)
; OTHER INFORMATION: SEPALLATA2 (SEP2)
; US-09-853-450-29

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Best Local Similarity 59.1%; Pred. No. 5.7e-25;
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QY 323 TTCTCCAAAGCGCCGCAACGGGCTCTCTGAAGAGCGGACGAGATCTCCGTCCTGTAC 382
DB 61 TTTCGAAAGGCTAGAGAAATGTTGCTGAAAAAGCTTATGAGCTTTCTCTGCGAT 120
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US-09-853-450-5

Query Match 26.4%; Score 156.6; DB 9; Length 768;
Best Local Similarity 67.1%; Pred. No. 6.8e-40;
Matches 222; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 263 ATGGTCCGCGCAAGTGTGAGCTGAAGCGGATGAGACAAATTAATGCGAGGTGACC 322
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QY 323 TTCTCCAAAGCCCGCAAGCGGGCTCCTGAAGAGGGGCAAGATCTCCGCTCTGTGAC 382
DB 61 TTCTGAAAAGAGAGCTGCTTTATGAAGAAAGCTCATGAGATCTCTGTCTGTGAT 120
QY 383 GCGGAGGTGCGCGGTATGCTCTTCTCCCAAGGCAAGCTCTATGATGACCCGAC 442
DB 121 GCTGAAGTTGGCGCTGTGTCTTCTCCCAAGGGAACCTTTGAATACCCCACTGAT 180
QY 443 TCCAGCATGACAAATTTTGAAGGTATGAGCGCTACTTTATGCTGAAGAGCTCTT 502
DB 181 TCTTATGAGAGAGATCTTGAAGCGTATGAGAGATCTTACGCCGAGAGACAGCTT 240
QY 503 ATTGAGCTGATCTGAAGAGTGAAGGAATTTGTCGACGATACAGAACTTAAGGCG 562
DB 241 ATGCACTGAGTCCGACTCCAAATGCAAGTGTGATGATATATGAGCTTAAGGCT 300
QY 563 AAGATTGAGACCATCAAAATATGTCAAGC 593
DB 301 AAGATTGAGCTTTTGAAGAGAAACGAGGCG 331

RESULT 10

US-09-853-450-9
Sequence 9, Application US/09853450
Publication No. US20020194645A1
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Pelaz, Soraya
APPLICANT: Ditlea, Gary
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
FILE REFERENCE: 19452A-002400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 779

TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (10)..(777)
OTHER INFORMATION: CAULIFLOWER (CAL)
NAME/KEY: modified base
LOCATION: (778)..(779)
OTHER INFORMATION: n = g, a, c or t

Query Match 24.5%; Score 145.2; DB 9; Length 779;
Best Local Similarity 66.5%; Pred. No. 3.1e-36;
Matches 226; Conservative 0; Mismatches 108; Indels 6; Gaps 1;

QY 260 GATATGGTCCGCGCAAGTGTGAGCTGAAGCGGATGAGACAAATTAATGCGAGGTG 319
DB 7 GAAATGGAGAGGGGTGAGTTGAATGAAGAGATGAGAACAAATCAATGACAGGTG 66
QY 320 ACCTTTCGAAGCGCGCAAGCGGCTCCTGAAGAGAGGCGACGAGATCTCCGCTCTGT 379
DB 67 ACATTTCTGAAAAGAGAGAGTGTCTTTTGAAGAAAGCTCAGGAGATCTCTGTCTTTGT 126
QY 380 GACGCGAGGTGCGCGGTATGCTTTCTCCCAAGGCAAGCTCTATGATGACGCGCAC 439

DB 127 GATGCGGAGGTTTCCCTTAATGTCTTCCCATTAAGGCAATTTGTTGAGATCTCT 186

QY 440 GACTCCAGATGACCAAAATCTTGAAGGTATGAGCGCTACTTATGCTGAAGAAAGCT 499

DB 187 GATTTTCATGAGAGAGAGTCTTGAAGCGCTACGAGAGTATTTCTTACCGCGAGAGAC 246

QY 500 CTATTTGAGTGAATCTGAAGAGTGAAGGA-----AATGATGCCAAGAAATACAGAA 553
DB 247 CTGATGACCTGACTCTCAGCTTAATGCAACAGAGAACTGTCATATGATGATGACAGG 306

QY 554 CTTAAGCGGAAGTTGAGACCATACAAATATGTCAAGC 593
DB 307 CTTAAGCGCAAGATTGAGCTTTTGAAGAGAAACCAAGGCG 346

RESULT 11

US-09-853-450-11
Sequence 11, Application US/09853450
Publication No. US20020194645A1
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Pelaz, Soraya
APPLICANT: Ditlea, Gary
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
FILE REFERENCE: 19452A-002400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 756
TYPE: DNA
ORGANISM: Brassica oleracea
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(756)
OTHER INFORMATION: CAULIFLOWER

Query Match 22.4%; Score 132.6; DB 9; Length 756;
Best Local Similarity 64.4%; Pred. No. 3.3e-32;
Matches 217; Conservative 0; Mismatches 114; Indels 6; Gaps 1;

QY 263 ATGGTCCGCGCAAGTGTGAGCTGAAGCGGATGAGAAACAAATTAATGCGAGGTGACC 322
DB 1 ATGGGAAGGGGTGAGGTTGAATGAAGAGATGAGAAACAAATCAACCAAGTGAAG 60

QY 323 TTCTCCAAAGCCCGCAAGCGGCTCCTGAAGAGCGGCAAGATCTCCGCTCTGTGAC 382
DB 61 TTCTGAAAAGAGAGCTGCTTTTGAAGAAAGCTCATGAGATCTCTGTCTGTGAT 120

QY 383 GCGGAGGTGCGCGGTATGCTCTTCTCCCAAGGCAAGCTCTATGATGACCCGAC 442
DB 121 GCTGAGGTTTCCCTTATGTTCTTCTCCCATAGGGAACCTTGAATGATCTCTGTGAA 180

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DB 181 TCTTCAATGAGAGAGTACTGAACACTACGAGAGTACTTTACGCCGAGAAACAGCTA 240

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DB 241 AAGTTCCAGCTCTCAGCTCAATGCAACAAAGAACTGTGATGATATATGAGAGGCTT 300

QY 557 AAGCGAAGATTGAGACCATCAAAATATGTCAAGC 593
DB 301 AAGCTTAAGATTGAGCTTTTGAAGAGAAACCAAGGCG 337

RESULT 12

US-09-853-450-13

OY 560 GCGAAGATTGAG 571
DB 398 GCAAGAGTTGAG 409

RESULT 7

US-09-978-740A-1
; Sequence 1, Application US/09978740A
; Publication No. US2003005481A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000960US
; CURRENT APPLICATION NUMBER: US/09/978,740A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(829)
; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-978-740A-1

Query Match 26.7%; Score 158.4; DB 9; Length 1062;
Best Local Similarity 69.2%; Pred. No. 2.1e-40;
Matches 216; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

OY 260 GATATGGTCCGCGCAAGTGTGAGCGGATGAGCAAGATTAATCGCAGGTG 319
DB 98 GATATGGAGAGAGTGGGTTTCACTGAGAGAGATGAGCAAGATTAATCGCAGGTG 157
OY 320 ACCTTCTCCAGCGCGCAAGCGGCTCTGAAAGAGGCGACGAGATCTCCGCTCTGT 379
DB 158 ACTTCTCAAGAGAGAGTGGGTTTCTGCTCAAGAGAGCTCATGAGATCTCTGCTGC 217
OY 380 GACGCGAGGTGCGCGTATGCTCTTCTCCCAAGGCAAGCTCTATGATGCGCAC 439
DB 218 GATGCTGAGTGGTCTCATGCTCTTCTTCCAAAGCAACTTGAATATTCAC 277
OY 440 GACTTCAGATGAGCAAAATTTGAAAGCTTATGAGCGGCTCTTATGCTGAAGAGCT 499
DB 278 GACTCTTCATGAGAGAGATCTTGAAGCTATGCTATGCTATTTATTCAGACAAACA 337
OY 500 CTATATTCAGTGAATCTGAAGAGTGAAGGAAATGCTGCAAGATGAGAACTTAAG 559
DB 338 CTGTTGGCCGAGAGCTTTTCAAAAGTGAATGGGTTTGAACAATGCTAAGCTCAAG 397
OY 560 GCGAAGATTGAG 571
DB 398 GCAAGAGTTGAG 409

RESULT 8

US-09-978-730-1
; Sequence 1, Application US/09978730
; Patent No. US20020129403A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic

; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000920US
; CURRENT APPLICATION NUMBER: US/09/978,730
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(829)
; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-978-730-1

Query Match 26.7%; Score 158.4; DB 10; Length 1062;
Best Local Similarity 69.2%; Pred. No. 2.1e-40;
Matches 216; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

OY 260 GATATGGTCCGCGCAAGTGTGAGCGGATGAGCAAGATTAATCGCAGGTG 319
DB 98 GATATGGAGAGAGTGGGTTTCACTGAGAGAGATGAGCAAGATTAATCGCAGGTG 157
OY 320 ACCTTCTCCAGCGCGCAAGCGGCTCTGAAAGAGGCGACGAGATCTCCGCTCTGT 379
DB 158 ACTTCTCAAGAGAGAGTGGGTTTCTGCTCAAGAGAGCTCATGAGATCTCTGCTGC 217
OY 380 GACGCGAGGTGCGCGTATGCTCTTCTCCCAAGGCAAGCTCTATGATGCGCAC 439
DB 218 GATGCTGAGTGGTCTCATGCTCTTCTTCCAAAGCAACTTGAATATTCAC 277
OY 440 GACTTCAGATGAGCAAAATTTGAAAGCTTATGAGCGGCTCTTATGCTGAAGAGCT 499
DB 278 GACTCTTCATGAGAGAGATCTTGAAGCTATGCTATGCTATTTATTCAGACAAACA 337
OY 500 CTATATTCAGTGAATCTGAAGAGTGAAGGAAATGCTGCAAGATGAGAACTTAAG 559
DB 338 CTGTTGGCCGAGAGCTTTTCAAAAGTGAATGGGTTTGAACAATGCTAAGCTCAAG 397
OY 560 GCGAAGATTGAG 571
DB 398 GCAAGAGTTGAG 409

RESULT 9

US-09-853-450-5
; Sequence 5, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Brassica oleracea var. botrytis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(768)
; OTHER INFORMATION: APETALA1 (AP1)

FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(829)
; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-978-729A-1

Query Match 26.7%; Score 158.4; DB 9; Length 1062;
Best Local Similarity 69.2%; Pred. No. 2.1e-40;
Matches 216; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 260 GATATGGGTCGGGCAAGGTGAGCTGAAAGCGGATAGAGAAAGTAAATGCGAGGTG 319
DB 98 GATATGGGAAAGAGGTGAGGTTCAGCTGAAGAGATAGAAACAAGTCAATAGGCAAGTT 157
QY 320 ACCCTTCACAGCGCGCAACCGGCTCTGAAAGAGCGCAGATCTCCGCTCTGT 379
DB 158 ACTTCTCAAGAGAGAGGTCTGTGTTGCTCAAGAAAGCTCAGATCTCTGTTCTGTC 217
QY 380 GACGCGAGGTGCGCGTCACTCTTCTCCCAAGGCAAGCTCTATGAGTACGCCACC 439
DB 218 GATGCTGAGGTGCTCTCATCTCTCTTCCAAAGGCAAGCTCTCGAATATTCACAC 277
QY 440 GACTCCAGATGACAAATTTGTAAGCTTATGAGCGCTACTCTTATGCTGAAGGCT 499
DB 278 GACTCTTGATGAGAGATGATCTGAAAGCTATGATCTATTTATTCAGACAAACA 337
QY 500 CTTATTTGAGCTGAATCTGAAAGTGAAGGAAATTTGGTCCAGCAATACAGAACTTAAG 559
DB 338 CTTGTTGGCCGAGAGCTTTCACAAAGTGAATTTGGTCTTGAACATGCTAAGCTCAAG 397
QY 560 GCGAAGATTGAG 571
DB 398 GCAAGAGTTGAG 409

RESULT 5

US-09-981-087A-1
; Sequence 1, Application US/09981087A
; Patent No. US20020178466A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; APPLICANT: Farrandiz, Cristina
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; FILE REFERENCE: 19452A-000940US
; CURRENT APPLICATION NUMBER: US/09/981,087A
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(829)
; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-981-087A-1

Query Match 26.7%; Score 158.4; DB 9; Length 1062;
Best Local Similarity 69.2%; Pred. No. 2.1e-40;
Matches 216; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 260 GATATGGGTCGGGCAAGGTGAGCTGAAAGCGGATAGAGAAAGTAAATGCGAGGTG 319
DB 98 GATATGGGAAAGAGGTGAGGTTCAGCTGAAGAGATAGAAACAAGTCAATAGGCAAGTT 157

QY 320 ACCCTTCACAGCGCGCAACCGGCTCTGAAAGAGCGCAGATTCGCTCTGT 379
DB 158 ACTTCTCAAGAGAGGTCTGTGTTGCTCAAGAAAGCTCATGATCTCTGTTCTGTC 217
QY 380 GACGCGAGGTGCGCGTCACTCTTCTCCCAAGGCAAGCTCTATGAGTACGCCACC 439
DB 218 GATGCTGAGGTGCTCTCATCTCTCTTCCAAAGGCAAGCTCTTGAATATTCACAC 277
QY 440 GACTCCAGATGACAAATTTGTAAGCTTATGAGCGCTACTCTTATGCTGAAGGCT 499
DB 278 GACTCTTGATGAGAGATGATCTGAAAGCTATGATCTTATTTATTCAGACAAACA 337
QY 500 CTTATTTGAGCTGAATCTGAAAGTGAAGGAAATTTGGTCCAGCAATACAGAACTTAAG 559
DB 338 CTTGTTGGCCGAGAGCTTTCACAAAGTGAATTTGGTCTTGAACATGCTAAGCTCAAG 397
QY 560 GCGAAGATTGAG 571
DB 398 GCAAGAGTTGAG 409

RESULT 6

US-09-978-382A-1
; Sequence 1, Application US/09978382A
; Publication No. US20020194647A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; FILE REFERENCE: 19452A-000930US
; CURRENT APPLICATION NUMBER: US/09/978,382A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(829)
; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-978-382A-1

Query Match 26.7%; Score 158.4; DB 9; Length 1062;
Best Local Similarity 69.2%; Pred. No. 2.1e-40;
Matches 216; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 260 GATATGGGTCGGGCAAGGTGAGCTGAAAGCGGATAGAGAAAGTAAATGCGAGGTG 319
DB 98 GATATGGGAAAGAGGTGAGGTTCAGCTGAAGAGATAGAAACAAGTCAATAGGCAAGTT 157
QY 320 ACCCTTCACAGCGCGCAACCGGCTCTGAAAGAGCGCAGATCTCCGCTCTGT 379
DB 158 ACTTCTCAAGAGAGAGGTCTGTGTTGCTCAAGAAAGCTCATGATCTCTGTTCTGTC 217
QY 380 GACGCGAGGTGCGCGTCACTCTTCTCCCAAGGCAAGCTCTATGAGTACGCCACC 439
DB 218 GATGCTGAGGTGCTCTCATCTCTCTTCCAAAGGCAAGCTCTTGAATATTCACAC 277
QY 440 GACTCCAGATGACAAATTTGTAAGCTTATGAGCGCTACTCTTATGCTGAAGGCT 499
DB 278 GACTCTTGATGAGAGATGATCTGAAAGCTATGATCTTATTTATTCAGACAAACA 337
QY 500 CTTATTTGAGCTGAATCTGAAAGTGAAGGAAATTTGGTCCAGCAATACAGAACTTAAG 559
DB 338 CTTGTTGGCCGAGAGCTTTCACAAAGTGAATTTGGTCTTGAACATGCTAAGCTCAAG 397

Oy	432	ACGCCACCCAGCTCCACAGATGGA	CAAAATCTTGAAGCTTATGAGGGCTACTTATCTG	491
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Oy	492	AAAAGGCTCTTATTTGAGCTGATCTG	AAAGTGAAGGAGAAATTTGGTCCACGATATACGA	551
Db	378	AAAAGGCTCTTATTTGAGCTGATCTG	AAAGTGAAGGAGAAATTTGGTCCACGATATACGA	437
Oy	552	AACCTAAAGCGAAGATTGAGACCAT	CAAAAAATGTCAACAG	593
Db	438	AACCTAAAGCGCAAAATTTGAGACCAT	CAAAAAATGTCCACAG	479

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RESULT 2
US-09-853-450-1
; Sequence 1, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; FILE REFERENCE: 19452a-002400US
; CURRENT APPLICATION NUMBER: US/09/853, 450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ-ID NOS: 61
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1057
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (124)..(894)
; OTHER INFORMATION: APETALA1 (Api)
US-09-853-450-1

Query Match: 27.6%; Score 163.4; DB 9; Length 1057;
Best Local Similarity 68.2%; Pred. No. 5.3e-42;
Matches 227; Conservative 0; Mismatches 106; Indels 0; Gaps 0

Db
261 ATATGGGTGCGCGCAAGGTGACGTGAGCGGATAGACAAGAATAATCGGAGGTGA 320
122 AAATGGGAAGGGGTAGCGGTCAATTGAAGAGATGAGAGACAAGATCAATAGACAAGTGA 181
321 CTTTCTCAAGCGCCGCAACGGGCTCTTGAAGAGCGGACGAGATCTCCGTCCTGTG 380
182 CATTCTCGAAAGAGAGAGCTGGCTTTTGAAGAAAGCTCATGAGATCTCTGTTCTGTG 241
361 ACGCGGAGGTGCGCGCTCATCGTCTTCTCCCCCAAAGGACAAGCTATAGTAGTACGCCACGC 440
242 ATGCTGAAGTTGCTCTGTGTTCTCTCCATTAAGGGGAAACCTTTCGAATACTCCACTG 301
441 ACTCAGCATGACAATAATTTCTGAAAGCTTATGAGGCGTACTCTTATGCTGAAAAGGCTC 500
302 ATTCTTGTATGGAAGAAAGATCACTTGAACGCTATGAGAGTACTCTTACGCCAAAGACAGC 361
501 TTATTTCACTGAATCTGAAAGTGAGGGGAAATTGGTGCCAGAAATACAGGAAACTTTAAG 560
362 TTATTGCACTGATAGTCCGACGTCAATACAAACCTGGTCATGATGATTAACAGGCTTAAG 421
561 CGAAGATTGAGACCATPACAAAATGTCAACAG 593
422 CTAAAGTTGAGCTTTTGGAGAGAACCAAGAGC 454

RESULT 3
US-09-853-450-3
; Sequence 3, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:

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APPLICANT: Yanofsky, Martin F.
 APPLICANT: Pelaz, Soraya
 APPLICANT: Ditta, Gary
 APPLICANT: The Regents of the University of California
 TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
 TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
 FILE REFERENCE: 19452A-002400US
 CURRENT APPLICATION NUMBER: US/09/853,450
 CURRENT FILING DATE: 2001-05-09
 NUMBER OF SEQ ID NOS: 61
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 3
 LENGTH: 794
 TYPE: DNA
 ORGANISM: Brassica oleracea
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (36)..(794)
 OTHER INFORMATION: ABETALAI (AP1)
 US-09-853-450-3

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Query March 26.7%: Score 158.6; DB 9; Length 794;
Best Local Similarity 67.3%; Pred. No. 1.6e-40;
Matches 224; Conservative 0; Mismatches 109; Indels 0; Gaps 0

Db 261 ATATGCTGCGCGCAAGGTGCAGCTGAGCGCGATAGAGACAAGATAAATCGCAGGTGA 320
34 AAATGGGAAGGGATAGAGGTTTCAGTTGAAGAGATAGAAAACAAGATCAATAGACAAGTGA 93
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Db 94 CATTCGAAAAGAAAGAGCTGGTCTTATGAAGAAAGCTCATGAGATCTCTGTCTGTGG 153
QY 381 ACGGGAGAGTGGCCGCTCATGCTCTTTCGCCCAAGGCAAGGCTATGAGTACGCGCACCG 440
Db 154 ATGCTGAAGTTGCGCTGTGTCTTCTTCCCATAGGGGAAATCTTTGAATATCTCACTG 213
QY 441 ACTCCAGCATGAGCAAAATTTCTTGAGCTTATGAGCGCTACTCTTATGCTGAAAAGCTC 500
Db 214 ATTCTTGATATGAGAAAGTACTTGAAGCGCTATGAGAGATCTTACGCCGAGAGACAGC 273
QY 501 TTATTTGAGCTGAATCTGTAAGATGAGGGAATTGGTGGCAGCAATATACAGAAAATTAAAG 560
Db 274 TTATAGCACTCGAGTGCAGCTCAATAGAACTGGTCATGAGATATATAGCTTAAAG 333
QY 561 CGAAGATTGAGACCATACAAAATGTCAACAGC 593
Db 334 CTAAGATTGAGCTTTGGAGAGAAAACAGAGGC 366

RESULT 4
US-09-978-729A-1
; Sequence 1, Application US/09978729A
; Patent No. US20020178465A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000950US
; CURRENT APPLICATION NUMBER: US/09/978,729A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.

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QY	252	GAAATTCAGATATGGGTCGGGCAAGGTGCAGCTGAAGCGGATAGAAACAAGTAATC	311
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QY	312	GGCAGGTACCTTCTCCAAAGCGCGCAAGGGGCTCTGAAGAAAGGCCACGAGATCTCCG	371
Db	198	GGCAGGTACCTTCTCCAAAGCGCGGAAAGCGCTCTCAAGAAAGGCCACGAGATCTCCG	257
QY	372	TCTCTGTAGCGGAGGTCGCGGTCATCGTCTTCTCCGCAAGGCAAGGCTATATAGT	431
Db	258	TCTCTGCGCATGCGAGGTGCGCGTCATCGTCTTCTCCGCAAGGCAAGGCTATATAGT	317

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DB 214 ATCTCTGATGAGAGAACTTGAAGCTTATAGAGAACTTGAAGCTTGAAGCTTGAAG 273
QY 501 TTATTTGAGCTGAATCTGAAAGTGAAGGAAATTTGTCGACGATATACAGAACTTAAAG 560
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DB 334 CTAAGATTGAGCTTTTGAAGAGAAACCAAGAGC 366

RESULT 15

US-08-659-188-3

Sequence 3, Application US/08659188

Patent No. 6002069

GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
TITLE OF INVENTION: Reproductive Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,188
FILING DATE: 05-JUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 794 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 36..794
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..794
OTHER INFORMATION: /note="product = Brassica oleracea
OTHER INFORMATION: APl."
US-08-659-188-3

Query Match

26.7%; Score 158.6; DB 3; Length 794;

Best Local Similarity 67.3%; Pred. No. 4e-35;

Matches 224; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

DB 34 AAATGGAGGGGTAGGCTTCATTTGAAGAGATAGAAAACAAGATCAATAGACAAGTGA 93
QY 321 CTTTCTCCAGCGCGGCAACGGGCTCTGAAAGAGCGCAGAGATCTCCGCTCTGTG 380
DB 94 CATTCTGAAAGAGAGAGCTGTCTTATGAAAGAGCTCAGATCTCTGTCTGTG 153
QY 381 ACGGAGAGTGGCCGTCATCTCTTCTCCCAAGGCAAGCTTATAGTACGCCACCG 440
DB 154 ATGCTGAAGTTGCGCTTGTGCTTCTCCCAATAGGGGAACTCTTGAATCTCACTG 213
QY 441 ACTCAGATGAGCAAAATCTTGAAGCTTATAGAGCGCTACTCTATCTGAAAAGGCTC 500
DB 214 ATCTCTGATGAGAGAACTTGAAGCTTATAGAGAACTTGAAGCTTGAAGCTTGAAG 273
QY 501 TTATTTGAGCTGAATCTGAAAGTGAAGGAAATTTGTCGACGATATACAGAACTTAAAG 560
DB 274 TTATAGCACTGAGCTGAGCTGCACTCCATATAGAACTGTCGATGAGATATATAGGCTTAAAG 333
QY 561 CGAAGATTGAGACCATACAAAATGTCAAGC 593
DB 334 CTAAGATTGAGCTTTTGAAGAGAAACCAAGAGC 366

Search completed: June 29, 2003, 07:26:47

Job time : 36 secs

TITLE OF INVENTION: Reproductive Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/398,326
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/659,188
FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 3739
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 124..893
NAME/KEY: misc feature
LOCATION: 1..1057
OTHER INFORMATION: /note="product = Arabidopsis
OTHER INFORMATION: thaliana Apl."
US-09-398-326-1

Query Match 27.6%; Score 163.4; DB 4; Length 1057;
Best Local Similarity 68.2%; Pred. No. 2e-36;
Matches 227; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

261 ATATGGGTGCGCGCAAGTGTGACGTGAGCGGATGAGACAAGTAATTCGGCAGGTGA 320
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321 CCTTCCAGGCGCGCAAGGCTCCGTAAGAGCGGACAGATCCCGTCTGTGTG 380
182 CATTTCTGAAAGAAAGAGCTGTCTTTGAGAAAGAGCTATAGATCTCTGTCTGTG 241
381 ACGCGAGGTGCGCGTCAATCTCTTCTCCCAAGGCAAGCTCTATGATGACGCAACG 440
242 ATGCTGAAGTGTCTGTGTCTCTCTCCCAAGGCAAGCTCTTCAATCTCTCACTG 301
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501 TTATTTCAGCTGAATCTGAAAGTGAAGGAAATTTGTTGCGACGAATACAGAAACTTAAG 560
362 TTATTGCACTGAGTCCAGCTCAATACAAAGCTGTGATGAGATTAACAGGCTTAAG 421
561 CGAAGATTGAGACATACAAATATGTCAACAGC 593
422 CTAGATTGAGCTTTTGGAGAGAAACAGAGGC 454

RESULT 12
US-08-592-214A-1
Sequence 1, Application US/08592214A
Patent No. 5811536
GENERAL INFORMATION:
APPLICANT: Vanofsky, Martin P.
TITLE OF INVENTION: Cauliflower Floral Meristem Identify
TITLE OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,214A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1927
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1215 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: join(141..905, 909..971, 975..1047)
NAME/KEY: misc feature
LOCATION: 1..1215
OTHER INFORMATION: /note="product = Arabidopsis
OTHER INFORMATION: thaliana Apl."
US-08-592-214A-1

Query Match 27.6%; Score 163.4; DB 1; Length 1215;
Best Local Similarity 68.2%; Pred. No. 2.2e-36;
Matches 227; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

261 ATATGGGTGCGCGCAAGTGTGACGTGAGCGGATGAGACAAGTAATTCGGCAGGTGA 320
139 AATGGGAAGGGGTGAGGTTCAATTGAGAGGATGAGACAAGTATAGACAAGTGA 198
321 CCTTCCAGGCGCGCAAGGCTCCGTAAGAGCGGACAGATCCCGTCTGTGTG 380
199 CATTTCTGAAAGAAAGAGCTGTCTTTGAGAAAGAGCTATGAGATCTCTGTCTGTG 258
381 ACGCGAGGTGCGCGTCAATCTCTTCTCCCAAGGCAAGCTCTATGATGACGCAACG 440
259 ATGCTGAAGTGTCTGTGTCTCTCTCCCAAGGCAAGCTCTTGAATATCTCACTG 318
441 ACTCAGCATGAGCAAAATTTCTTGAAGCTTATGAGCGCTACTCTTATGCTGAAAAGGCTC 500
319 ATTTCTTATGAGAAAGATTAAGTGAAGCTATGAGAGGTAAGCTTACCGCGAAAGACAGC 378
501 TTATTTCAGCTGAATCTGAAAGTGAAGGAAATTTGTTGCGACGAATACAGAAACTTAAG 560
379 TTATTGCACTGAGTCCAGCTCAATACAAAGCTGTGATGAGATTAACAGGCTTAAG 438

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,227
FILING DATE: 05-JUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2143
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 124..893
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1057
OTHER INFORMATION: /note= "product = Arabidopsis
OTHER INFORMATION: thaliana Apl."
US-08-655-227-1

Query Match 27.6%; Score 163.4; DB 3; Length 1057;
Best Local Similarity 68.2%; Pred. No. 2e-36;
Matches 227; Conservative 0; Mismatches 106; Indels 0; Gaps 0;
DB 261 ATATGGTTCGCGGAGGTCAGCTGAAGCGGATGAGAAACAATAATCGGAGGTGA 320
122 AAATGGGAAGGGGTGAGGTTCAATTGAGAGATGAGAGACAGATCATTAGACAGTGA 181
QY 331 CTTTCTCAAGCGCGCAACGGGCTCTGAAGAGCGGACAGATCTTCCGCTCTGTG 380
182 CATCTCGAAGAGAGAGCTGTCTTTGAAGAAAGCTCATGATCTCTGTCTGTG 241
DB 381 ACGGAGAGTCCCGTCATCTCTTCTCCCAAGGCAAGCTCATGAGTACGACCG 440
242 ATGCTGAAGTTGCTCTTGTGCTCTCTCCATAGGGGAACTCTTCGATCTCCACTG 301
QY 441 ACTCCAGATGAGCAAAATTTGAAAGTTATGAGGCTACTTATGCTGAAAAGGCTC 500
302 ATTCTGTATGAGAGATGACTTGAACGCTATGAGAGGTACTCTTAAGCGGAAAGACG 361
DB 501 TTATTTAGCTGAATCTGAAGTGAAGGAAATTGTGCGACGATACAGAAACTTAAG 560
362 TTATTTAGCACTGAGTCCGACGTCAATACAACTGGTGCATGAGATATAACAGCTTAAG 421
QY 561 CGAAGATTGAGACCATACAAAATGTCAACAGC 593
422 CTAAAGATTGAGCTTTTGGAGAGAAACCAAGAGC 454
DB

RESULT 10
US-08-655-241-1
Sequence 1, Application US/08655241
Patent No. 6025543
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Weigelt, Detlef
TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
NUMBER OF SEQUENCES: 26
DEVELOPMENT AND METHODS OF MAKING SAME
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,241
FILING DATE: 05-JUN-1996
CLASSIFICATION: CLASS 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1894
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 124..893
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1057
OTHER INFORMATION: /note= "product = Arabidopsis
OTHER INFORMATION: thaliana Apl."
US-08-655-241-1

Query Match 27.6%; Score 163.4; DB 3; Length 1057;
Best Local Similarity 68.2%; Pred. No. 2e-36;
Matches 227; Conservative 0; Mismatches 106; Indels 0; Gaps 0;
DB 261 ATATGGTTCGCGGAGGTCAGCTGAAGCGGATGAGAAACAATAATCGGAGGTGA 320
122 AAATGGGAAGGGGTGAGGTTCAATTGAGAGATGAGAGACAGATCATTAGACAGTGA 181
QY 331 CTTTCTCAAGCGCGCAACGGGCTCTGAAGAGCGGACAGATCTTCCGCTCTGTG 380
182 CATCTCGAAGAGAGAGCTGTCTTTGAAGAAAGCTCATGAGATCTCTGTCTGTG 241
DB 381 ACGGAGAGTCCCGTCATCTCTTCTCCCAAGGCAAGCTCATGAGTACGACCG 440
242 ATGCTGAAGTTGCTCTTGTGCTCTCTCCATAGGGGAACTCTTCGATCTCCACTG 301
QY 441 ACTCCAGATGAGCAAAATTTGAAAGTTATGAGGCTACTTATGCTGAAAAGGCTC 500
302 ATTCTGTATGAGAGATGACTTGAACGCTATGAGAGGTACTCTTAAGCGGAAAGACG 361
DB 501 TTATTTAGCTGAATCTGAAGTGAAGGAAATTGTGCGACGATACAGAAACTTAAG 560
362 TTATTTAGCACTGAGTCCGACGTCAATACAACTGGTGCATGAGATATAACAGCTTAAG 421
QY 561 CGAAGATTGAGACCATACAAAATGTCAACAGC 593
422 CTAAAGATTGAGCTTTTGGAGAGAAACCAAGAGC 454
DB

RESULT 11
US-09-398-326-1
Sequence 1, Application US/09398326
Patent No. 635863
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early

OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/576,156
FILING DATE: 12-21-95
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,336
FILING DATE: 12-21-94
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07251/013001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1054
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-576-156-1

Query Match 27.6%; Score 163.4; DB 2; Length 1054;
Best Local Similarity 68.2%; Pred. No. 2e-36;
Matches 227; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

261 ATATGGGTGCGGCAAGTGTGACGCTGAGCGATAGAGAAACAATAATCGGAGGTGA 320
122 AATGGAAGAGGGTGGTGGTCAATTGAAAGAGATGAGAAACAAGATCAATAGACAAGTGA 181
321 CCTTCTCCAGGCGCGCAACGGGCTCTGTAAGAGCGCAGAGATCTCCGTCTCTGTG 380
182 CATTCGAAAGAGAGAGTGTGCTTTTGAAGAAAGCTATGATCTCTGTTCTGTG 241
381 ACGGGAAGTGGCCGTCATGCTCTTCTCCCAAGAGCAAGCTTATGAGTACGCCACCG 440
242 ATGCTGAAGTGTCTGTTGTTCTCTCCATTAAGGGGAAACTCTTCGAACTACCTCAGTG 301
441 ACTCAGATGAGCAAAATTTCTGAACGTTATGAGCGCTACTCTTATGCTGAAAAGGCTC 500
302 ATCTCTGATGAGAAAGATCTTGAACGCTATGAGAGGTACTTTAAGCGGAAAGACAGC 361
501 TTATTTAGCTGAATCTGAAAGTGAAGGAAATTGTGCGACGATATACAGAACTTAAAG 560
362 TTATTTGACCTGAGTCCGACGCTCAATACAACTGTCGATGAGATTAACAGGCTTAAAG 421
561 CGAAGATTGAGACCATACAAAATGTCAACAGC 593
422 CTAAGATTGAGCTTTTGGAGAGAAACCAAGAGC 454

RESULT 8
US-08-659-188-1
Sequence 1, Application US/08659188
Patent No. 6002069

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
TITLE OF INVENTION: Reproductive Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA

ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,188
FILING DATE: 05-JUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 124..893
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1057
OTHER INFORMATION: /note="product = Arabidopsis
OTHER INFORMATION: thaliana ABI."
US-08-659-188-1

Query Match 27.6%; Score 163.4; DB 3; Length 1057;
Best Local Similarity 68.2%; Pred. No. 2e-36;
Matches 227; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

261 ATATGGGTGCGGCAAGTGTGACGCTGAGCGATAGAGAAACAATAATCGGAGGTGA 320
122 AATGGAAGAGGGTGGTGGTCAATTGAAAGAGATGAGAAACAAGATCAATAGACAAGTGA 181
321 CCTTCTCCAGGCGCGCAACGGGCTCTGTAAGAGCGCAGAGATCTCCGTCTCTGTG 380
182 CATTCGAAAGAGAGTGTGCTTTTGAAGAAAGCTATGAGATCTCTGTTCTGTG 241
381 ACGGGAAGTGGCCGTCATGCTCTTCTCCCAAGCAAGCTTATGAGTACGCCACCG 440
242 ATGCTGAAGTGTCTGTTGTTCTCTCCATTAAGGGGAAACTCTTCGAACTACCTCAGTG 301
441 ACTCAGATGAGCAAAATTTCTGAACGTTATGAGCGCTACTCTTATGCTGAAAAGGCTC 500
302 ATCTCTGATGAGAAAGATCTTGAACGCTATGAGAGGTACTTTAAGCGGAAAGACAGC 361
501 TTATTTAGCTGAATCTGAAAGTGAAGGAAATTGTGCGACGATATACAGAACTTAAAG 560
362 TTATTTGACCTGAGTCCGACGCTCAATACAACTGTCGATGAGATTAACAGGCTTAAAG 421
561 CGAAGATTGAGACCATACAAAATGTCAACAGC 593
422 CTAAGATTGAGCTTTTGGAGAGAAACCAAGAGC 454

RESULT 9
US-08-655-227-1
Sequence 1, Application US/08655227
Patent No. 6025483

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Maize and Cauliflower APETALA1 Gene
TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA

ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 149..968
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1345
OTHER INFORMATION: /note= "product = Zea mays APL"
US-09-149-976-7

Query Match: 50.7%; Score 300.4; DB 3; Length 1345;
Best Local Similarity 92.4%; Pred. No. 1.3e-74;
Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 252 GAATCAGATATGGGTGCGCGCAAGTGCAGCTGAGCGGATGAGAACAGATTAATC 311
DB 138 GCAACAGGCGATGGGGCGCGCAAGTGCAGCTGAGCGGATGAGAACAGATTAATC 197
QY 312 GCGAGTGAACCTTCTCCAAAGCGCGCAAGCGGCTCTGAGAAAGCGCGAGATCTCG 371
DB 198 GCGAGTGAACCTTCTCCAAAGCGCGCAAGCGGCTCTGAGAAAGCGCGAGATCTCG 257
QY 372 TCCTGTGAGCGCGAGGTGCGCGTCAATGCTTCTCCCGCAAGCGAGCTCTATGCTG 431
DB 258 TCCTGTGAGCGCGAGGTGCGCGTCAATGCTTCTCCCGCAAGCGAGCTCTATGCTG 317
QY 432 ACGCCACGACTCCAGATGAGCAAAATTTCTTGAAGCGGCTACTCTTATGCTG 491
DB 318 ACGCCACGACTCCAGATGAGCAAAATTTCTTGAAGCGGCTACTCTTATGCTG 377
QY 492 AAAAGGCTTTATTTCACTGATGTAATCTGAAAGTGAGGAAATTTGTCGCAATACAGA 551
DB 378 AAAAGGCTTTATTTCACTGATGTAATCTGAAAGTGAGGAAATTTGTCGCAATACAGA 437
QY 552 AACTTAAGCGGAAGTTGAGACCATACAAATATGTCACAGC 593
DB 438 AACTGAAGCCAAATTTGAGACCATACAAATATGTCACAGC 479

RESULT 6

US-09-398-326-7
Sequence 7, Application US/09398326
Patent No. 6355863

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
TITLE OF INVENTION: Reproductive Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESS: Campbell and Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/398,326

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/659,188
FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 3739
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 149..968
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1345
OTHER INFORMATION: /note= "product = Zea mays APL."
US-09-398-326-7

Query Match: 50.7%; Score 300.4; DB 4; Length 1345;
Best Local Similarity 92.4%; Pred. No. 1.3e-74;
Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 252 GAATCAGATATGGGTGCGCGCAAGTGCAGCTGAGCGGATGAGAACAGATTAATC 311
DB 138 GCAACAGGCGATGGGGCGCGCAAGTGCAGCTGAGCGGATGAGAACAGATTAATC 197
QY 312 GCGAGTGAACCTTCTCCAAAGCGCGCAAGCGGCTCTGAGAAAGCGCGAGATCTCG 371
DB 198 GCGAGTGAACCTTCTCCAAAGCGCGCAAGCGGCTCTGAGAAAGCGCGAGATCTCG 257
QY 372 TCCTGTGAGCGCGAGGTGCGCGTCAATGCTTCTCCCGCAAGCGAGCTCTATGCTG 431
DB 258 TCCTGTGAGCGCGAGGTGCGCGTCAATGCTTCTCCCGCAAGCGAGCTCTATGCTG 317
QY 432 ACGCCACGACTCCAGATGAGCAAAATTTCTTGAAGCGGCTACTCTTATGCTG 491
DB 318 ACGCCACGACTCCAGATGAGCAAAATTTCTTGAAGCGGCTACTCTTATGCTG 377
QY 492 AAAAGGCTTTATTTCACTGATGTAATCTGAAAGTGAGGAAATTTGTCGCAATACAGA 551
DB 378 AAAAGGCTTTATTTCACTGATGTAATCTGAAAGTGAGGAAATTTGTCGCAATACAGA 437
QY 552 AACTTAAGCGGAAGTTGAGACCATACAAATATGTCACAGC 593
DB 438 AACTGAAGCCAAATTTGAGACCATACAAATATGTCACAGC 479

RESULT 7

US-08-576-156-1
Sequence 1, Application US/08576156
Patent No. 5844119

GENERAL INFORMATION:

APPLICANT: Weigelt, Detlef
TITLE OF INVENTION: Genetically Modified Plants Having Modulated
TITLE OF INVENTION: Flower Development
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..1345
OTHER INFORMATION: /note= "product = Zea mays APL."
US-08-655-227-7

Query Match 50.7%; Score 300.4; DB 3; Length 1345;
Best Local Similarity 92.4%; Pred. No. 1.3e-74;
Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

252 GAAATCAGATATGATGCGCGGCAAGTGCAGCTGAAGCGGATAGAGAACAAGATAATC 311
138 GCAACAAAGCCATGGGGCGCGGCAAGTACAGCTGAAGCGGATAGAGAACAAGATAAAC 197
312 GCGAGTGACCTTCTCCAAAGCGCGCAACGGGCTCTTGAAGAGCGACGAGATCTCG 371
198 GCGAGTGACCTTCTCCAAAGCGCGGAAAGGCTCTCTCAAGAGCGGACGAGATCTCG 257
372 TCCTGTGAGCGCGGAGGTGCGCGCTCATGCTTTCTCCCGCAAGCGCAAGCTCTATGAGT 431
258 TCCTGTGAGATGCGGAGGTGCGCGCTCATGCTTTCTCCCGCAAGCGCAAGCTCTATGAGT 317
432 ACGCACCGACTCCGAGATGAGCAAAATTTGAAAGTTATGAGGCGTACTTATGCTG 491
318 ACGCACCGACTCCGAGATGAGCAAAATTTGAAAGTTATGAGGCGTACTTATGCTG 377
492 AAAAGGCTCTTATTTCACTGAATCTGAAGTGAAGGAAATTTGTCGACGATACAGA 551
378 AAAAGGCTCTTATTTCACTGAATCTGAAGTGAAGGAAATTTGTCGACGATACAGA 437
552 AACTTAAGCGCAAGTTGAGACCATACAAAATGTCACAGC 593
438 AACTGAAGGCCAAATTAAGACCATACAAAATGTCACAGC 479

RESULT 4

US-08-655-241-7
Sequence 7, Application US/08655241
Patent No. 6025543
GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.
APPLICANT: Weigel, Detlef
TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
TITLE OF INVENTION: Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA

ZIP: 92122
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/655,241

FILING DATE: 05-JUN-1996

CLASSIFICATION: CLASS 800

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 1894

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1345 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 149..968
FEATURE:

NAME/KEY: misc_feature
LOCATION: 1..1345
OTHER INFORMATION: /note= "product = Zea mays APL."
US-08-655-241-7

Query Match 50.7%; Score 300.4; DB 3; Length 1345;
Best Local Similarity 92.4%; Pred. No. 1.3e-74;
Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

252 GAAATCAGATATGATGCGCGGCAAGTGCAGCTGAAGCGGATAGAGAACAAGATAATC 311
138 GCAACAAAGCCATGGGGCGCGGCAAGTACAGCTGAAGCGGATAGAGAACAAGATAAAC 197
312 GCGAGTGACCTTCTCCAAAGCGCGCAACGGGCTCTTGAAGAGCGGACGAGATCTCG 371
198 GCGAGTGACCTTCTCCAAAGCGCGGAAAGGCTCTCTCAAGAGCGGACGAGATCTCG 257
372 TCCTGTGAGCGCGGAGGTGCGCGCTCATGCTTTCTCCCGCAAGCGCAAGCTCTATGAGT 431
258 TCCTGTGAGATGCGGAGGTGCGCGCTCATGCTTTCTCCCGCAAGCGCAAGCTCTATGAGT 317
432 ACGCACCGACTCCGAGATGAGCAAAATTTGAAAGTTATGAGGCGTACTTATGCTG 491
318 ACGCACCGACTCCGAGATGAGCAAAATTTGAAAGTTATGAGGCGTACTTATGCTG 377
492 AAAAGGCTCTTATTTCACTGAATCTGAAGTGAAGGAAATTTGTCGACGATACAGA 551
378 AAAAGGCTCTTATTTCACTGAATCTGAAGTGAAGGAAATTTGTCGACGATACAGA 437
552 AACTTAAGCGCAAGTTGAGACCATACAAAATGTCACAGC 593
438 AACTGAAGGCCAAATTAAGACCATACAAAATGTCACAGC 479

RESULT 5

US-09-149-976-7
Sequence 7, Application US/09149976
Patent No. 6127123
GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.
APPLICANT: Genes and Methods of Using Same
TITLE OF INVENTION: Cauliflower Floral Meristem Identity
TITLE OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States

ZIP: 92122
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/149,976

FILING DATE: 09-SEP-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/592,214

FILING DATE: 26-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 3291

TELECOMMUNICATION INFORMATION:

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2003, 07:25:59 ; Search time 1068 Seconds
(without alignments)
8992.438 Million cell updates/sec

Title: US-10-020-338-8

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Optimal number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_esthm:*
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27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	421.8	71.1	567	13	BJ207882 BJ207882
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9	385.4	65.0	1658	13	BJ213269
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27	259.8	43.8	543	13	BM374839
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34	255	43.0	497	12	BE624256
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36	253.4	42.7	832	12	BG343946
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40	228.8	38.6	488	9	AJ432143
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ALIGNMENTS

RESULT 1
LOCUS BJ208073 633 bp mRNA linear EST 04-APR-2002
DEFINITION BJ208073 Y. Ogihara unpublished cDNA library, wh Triticum aestivum
CDNA clone wh6110 5', mRNA sequence.
ACCESSION BJ208073
VERSION BJ208073.1 GI:19946124
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticaceae; Triticum.
REFERENCE
1 (bases 1 to 633)
Ogihara, Y. and Mural, K.
Expressed genes in Triticum aestivum
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.

FEATURES

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1..633
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"

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/clone="whb110"
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Site_1: EcoRI, Site_2: XhoI. Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J. Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give plasmid phagemids in the TV Close lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."

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Query Match	86.7%	Score 514.2	DB 13	Length 633
Best Local Similarity	99.4%	Pred No. 1.4e-122		
Matches 516	Conservative 0	Mismatches 3	Indels 0	Gaps 0

Oy 75 CGACACTGCATCGCAGCCCTCCGCCCAATTACAGCAAAATGCATCGCTCTTCTCTCC 134
 Db 1 CGAGGCTGCATCGCAGCCCTCCGCCCAATTACAGCAAAATGCATCGCTCTTCTCTCC 60

QY 135 CATCTTTAAGCTGTCATCCCATCTCCCTACCGCGCGGGGAGGACGACAGCATGTCTGCC 194

Db 61 CATCTTTAAGCTGTCATCCCATCTCCCTACCGCGCGGGGAGGACGACAGCATGTCTGCC 120

QY	Db
199	TTCCTCCACCCCGCGCGCGTGGCGGCCAATAGACACAAGAGCCGACAGCTAGATGCGGAA 254
121	TTCCTCCACCCCGCGCGCGTGGCGGCCAATAGACACAAGAGCCGACAGCTAGATGCGGAA 180

QY	255	ATCAGGATATGGGTCGGCGGCAAGTCAGCTGAACCGGATAGAGAACAAATTAATTCGGC	314
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QY	315	AGGAGCCTTCTCCAGGCGCGACGGGCTCTAAGAAAGGCGACGAATCTCCGTC	374
Db	241	AGGAGCCTTCTCCAGGCGCGACGGGCTCTAAGAAAGGCGACGAATCTCCGTC	300

QY	375	TCTGTGACGCGGAGTTCGCCGTCATCTCTTCTCCCCCAAAGGCAAGCTCTATGACTAC	434
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y	435	CCACCGCCTCCAGCATGGACAAATTTCTTGACGTTATGAGCGCTACTCTTATGCTGAAA	494
Db	361	CCACCGACTCCAGCATGGACAAATTTCTTGACGTTATGAGCGCTACTCTTATGCTGAAA	420

OY	495	AGGCTCTTATTTTCAGCTGAACTCTGAAAGTGAGGAAATTTGGTCCACGAATTACAGGAAC	554
Db	421	AGGCTCTTATTTTCAGCTGAACTCTGAAAGTGAGGAAATTTGGTCCACGAATTACAGGAAC	480

OY	555	TTAAAGCGAATTGAGACCATACAAAAATGTCAAGC	593
Dp	481	TTTAAGCCGAAGATTGAGACCATAAAAAAGTCACAGC	519

RESULT 2

ACCESSION	R1207882		
CDNA clone	wh5m21 5', mRNA sequence.		
DEFINITION	Bj207882 Y. Ogihara unpublished cDNA library, Wh	Triticum aestivum	
LOCUS	Bj207882	567 bp	linear
LOCUS	Bj207882	mRNA	EST 04-APR-2003

ORGANISM	<i>Triticum aestivum</i>
SOURCE	bread wheat.
KEYWORDS	EST.
VERSION	BJ207882.1
GI:19945861	

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae

REFERENCE : Triticeae; Triticum.
1 (bases 1 to 567)
AUTHORS Ogihara, Y. and Mouri, K.
TITLE Expressed genes in *Triticum aestivum*
JOURNAL Unpublished (2002)
COMMENT Contact: Tadashi Shin-I
C. D. C. Sci. Inform. Inform. Information

Center for Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp,
tshin@nig.ac.jp

FEATURES	Location/Qualifiers
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/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db xref="taxon:4565"
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(etc...) library=Oxphos_mitochondrion CDNA library
wh=
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/note=Vector: Lambda Uni-ZAP XR excised phagemid:
Site_1: EcoRI; Site_2: XhoI; Plants were grown under
hydropnic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J. Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pluescript phagemids in the T7 Close lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Kitanian, Otero, Simons, Zhang) .
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors). "

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BASE COUNT	ORIGIN
157 a	155 c
147 g	108 t

Query Match	71.1%	Score 421.8	DB 13	length 567
Best Local Similarity	99.1%	Pred. NO. 1.2e-98		
Matches 435; Conservative	0	Mismatches 2	Indels 2	Gaps 1

QY 155 ATCTCCCTCACCAGCGCGGCGAGCCAGCAGCTCTGCGCTCTCTCCACCCCGGCGCGG 214

Db 1 ATCTCCCTCACCAGCGCGGCGAGCCAGCAGCTCTGCGCTCTCTCCACCCCGGCGCGG 60

QY 215 TGGCGCCATAGACACAAGAGCCGACAGCTAGATCGCGAATATAGGATATGGGTGCGGC 274

Db 61 TGGCGCCATAGACACAAGAGCCGACAGCTAGATCGCGAATATAGG -- ATGGGTGCGGC 118

OY 275 AAGGTGACGCTGAAGCGGATAGAGAACAAATTAATCGGACGCTGACCTTCTCCAAAGCCC 334
 119 AAGGTGACGCTGAAGCGGATAGAGAACAAATTAATCGGACGCTGACCTTCTCCAAAGCCC 178
 Db

QY 335 CGCAACGGGCTCCTGAAAGAGCGCACGAGATCTCCGTTCTGTGTGACGCGAGGTCCGC 394

Db 179 CGCAACGGGCTCCTGAAAGAGCGCACGAGATCTCCGTTCTGTGTGACGCGAGGTCCGC 238

395 GTCATCGTCTTCCCCCAAGCCTATAGTAGTACGCCACGACTCCAGCATGAC 454
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455 AAAATTCGTAAAGCCTTATGCTGAAGAAGCCTTATTTGAGCTGA 514

0y 515 TCTGAAAGTGAGGGAAATTTGGTCCACAGATACAGAAACTTAAGCGCAAGATTGAGACC 574
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OY 575 ATACAAAATGTCACAAGC 593
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RESULT 3
BJ304647 716 bp mRNA linear EST 09-APR-2002
LOCUS BJ304647
DEFINITION BJ304647 Y. Ogihara unpublished cDNA library, Wh_yd Triticum
aestivum cDNA clone whyd7c05 5', mRNA sequence.
ACCESSION BJ304647
VERSION BJ304647.1 GI:20114624
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticaceae; Triticum.
1 (bases 1 to 716)
Ogihara,Y. and Murai,K.
Expressed genes in Triticum aestivum
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers
1. 716
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/cultivar="Chinese Spring"
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/dev_stage="Feekes' scale 6"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give plasmid phagemids in the TV Close lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."

BASE COUNT 210 a 190 c 200 g 116 t
ORIGIN
Query Match 71.1%; Score 421.4; DB 13; Length 716;
Best Local Similarity 99.3%; Pred. No. 1.6e-98;
Matches 434; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 157 CTCCCTACCGCGCGCGGCGAGCGACGCTCTCTCCACCCCGCGCGGTG 216
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QY 217 CGCGCATTAGACAAAGCGCGACGCTAGTCCGGAATAGATGGTCCGGCAA 276
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QY 457 AATCTTGAACGTTATGAGCGCTACTTATGCTGAAGAGCTTATTTACGCTGATC 516
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DB 318 AATCTTGAACGTTATGAGCGCTACTTATGCTGAAGAGCTTATTTACGCTGATC 377
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QY 517 TGAAGTGAAGAAATTGGTCCACGATATCAGGAACCTTAAAGCGGAATGACCAT 576
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DB 378 TGAAGTGAAGAAATTGGTCCACGATATCAGGAACCTTAAAGCGGAATGACCAT 437
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QY 577 ACAAAATGTCACAGC 593
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DB 438 ACAAAATGTCACAGC 454
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RESULT 4
BE500707 492 bp mRNA linear EST 04-AUG-2000
LOCUS BE500707
DEFINITION WHE0991-0994_121_121S wheat pre-anthesis spike cDNA library
Triticum aestivum cDNA clone WHE0991-0994_121_121, mRNA sequence.
ACCESSION BE500707
VERSION BE500707.1 GI:9699324
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticaceae; Triticum.
1 (bases 1 to 492)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
,P.S., Hala,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
Seaton,C.L. and Tong,J.C:
The structure and function of the expressed portion of the wheat
genomes - Pre-anthesis spike cDNA library
Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: anders@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: StrataGene SK primer.
Location/Qualifiers
1. 492
/organism="Triticum aestivum"
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/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
greenhouse. Whole spike with awns trimmed. White, green
and yellow anther were collected and total RNA, and
poly(A) RNA were prepared, a cDNA library was made, and
the cDNA clones were in vivo excised to give plasmid
phagemids in the TV Close lab (Choi, Close, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

BASE COUNT 140 a 131 c 128 g 93 t
ORIGIN
Query Match 67.8%; Score 402; DB 10; Length 492;
Best Local Similarity 99.8%; Pred. No. 1.5e-93;
Matches 413; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 180 CAGCAGCTCTCCCTCTCCACCCCGCGCGCGCGCATGACAAAGAGCGA 239
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Db 2 CAGGACGCTCGCTCTCTCC-CCCCGCGCGCGCCCATAGACACAGAGCCGA 60
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 Db 121 ACAAGATTAATCGCAGAGTGAACCTTCTCCAGCCGCGCAAGCGGCTCTGTAAGAGCGC 180
 QY 360 ACGAGATCTCCGCTCTCTGTGACGCGAGTCCGCTGATCTCTTCTCCCAAGCA 419
 Db 181 ACGAGATCTCCGCTCTCTGTGACGCGAGTCCGCTGATCTCTTCTCCCAAGCA 240
 QY 420 AGCTTATGATGACGCGACCTCCAGCATGAGCAAAATCTTGAAGTATAGAGCT 479
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 QY 480 ACTCTTATGCTGAAAAGGCTCTTATTTGAGCTGATGAAAGTGAAGGAATTGTGCC 539
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 QY 540 ACGAATACAGAACTTAAGCGGAAGATTGAGACCATACAAAATGTCAAGC 593
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RESULT 5 555 bp mRNA linear EST 16-APR-2001
 BG605208
 LOCUS
 DEFINITION WHE2330 A04 A0825 wheat pre-anthesis spike cDNA library Triticum
 accession BG605208
 VERSION
 KEYWORDS
 SOURCE
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 Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
 ; Triticaceae; Triticum.
 1 (bases 1 to 555)
 Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han
 P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,
 Seaton, C.L. and Tong, J.C.
 The structure and function of the expressed portion of the wheat
 genomes - Pre-anthesis spike cDNA library
 Unpublished (2000)
 CONTACT: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818
 Email: oanderson@wp.usda.gov
 Sequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: Stragene SK primer.
 Location/Qualifiers
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 /organism="Triticum aestivum"
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 /dev_stage="Adult plant"
 /lab_host="E. coli SOLR"
 /note="vector: lambda Uni-ZAP XR, excised phagemid;
 Site 1: EcoRI, Site 2: XhoI; Plants were grown in the
 greenhouse. Whole spike with awns trimmed, white, green
 and yellow anther were collected and total RNA, and
 poly(A) RNA were prepared, a cDNA library was made, and
 the cDNA clones were in vivo excised to give pluescript

BASE COUNT 161 a 143 c 147 g 104 t
 ORIGIN
 Query Match 66.6%; Score 395.2; DB 12; Length 555;
 Best Local Similarity 98.8%; Pred. No. 8.9e-92;
 Matches 409; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
 phagemids in the TJ Close lab (Choi, Close, Fenton) at
 the University of California, Riverside. Plasmid DNA
 preparations and DNA sequencing were performed in the OD
 Anderson lab (all other authors)."

Db 180 CAGGACGCTCGCTCTCTCCACCCGCGCGCGCCCATAGACACAGAGCCGA 239
 Db 1 CAGGACGCTCGCTCTCTCCACCCGCGCGCGCCCATAGACACAGAGCCGA 60
 QY 240 CAGTATATGCGGAATAGATATGAGTCCGCGGAGAGTACGTAGAGGATAGAGA 299
 Db 61 CAGTATATGCGGAATAGATATGAGTCCGCGGAGAGTACGTAGAGGATAGAGA 120
 QY 300 ACAAGATTAATCGCAGAGTGAACCTTCTCCAGCCGCGCAAGCGGCTCTGTAAGAGCGC 359
 Db 121 ACAAGATTAATCGCAGAGTGAACCTTCTCCAGCCGCGCAAGCGGCTCTGTAAGAGCGC 180
 QY 360 ACGAGATCTCCGCTCTCTGTGACGCGAGTCCGCTGATCTCTTCTCCCAAGCA 419
 Db 181 ACGAGATCTCCGCTCTCTGTGACGCGAGTCCGCTGATCTCTTCTCCCAAGCA 240
 QY 420 AGCTTATGATGACGCGACCTCCAGCATGAGCAAAATCTTGAAGTATAGAGCT 479
 Db 241 AGCTTATGATGACGCGACCTCCAGCATGAGCAAAATCTTGAAGTATAGAGCT 300
 QY 480 ACTCTTATGCTGAAAAGGCTCTTATTTGAGCTGATGAAAGTGAAGGAATTGTGCC 539
 Db 301 ACTCTTATGCTGAAAAGGCTCTTATTTGAGCTGATGAAAGTGAAGGAATTGTGCC 360
 QY 540 ACGAATACAGAACTTAAGCGGAAGATTGAGACCATACAAAATGTCAAGC 593
 Db 361 ACGAATACAGAACTTAAGCGGAAGATTGAGACCATACAAAATGTCAAGC 414

RESULT 6 691 bp mRNA linear EST 09-APR-2002
 BJ316394
 LOCUS
 DEFINITION BJ316394 Y. Ogihara unpublished cDNA library, wh_yf Triticum
 accession BJ316394
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
 ; Triticaceae; Triticum.
 1 (bases 1 to 691)
 Ogihara, Y. and Murai, K.
 Expressed genes in Triticum aestivum
 Unpublished (2002)
 CONTACT: Tadasu Shin-i
 Center for Genetic Resource Information
 National Institute of Genetics
 111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tehin@genes.nig.ac.jp.
 Location/Qualifiers
 1..691
 /organism="Triticum aestivum"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="whyf22009"
 /clone_lib="Y. Ogihara unpublished cDNA library, wh_yf"
 /tissue_type="spikelet at early flowering"
 /dev_stage="Peekes' scale 6"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J. Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give plasmid phagemids in the T7 Close Lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."

BASE COUNT 210 a 179 c 189 g 113 t
ORIGIN

Query Match 66.6%; Score 394.8; DB 13; Length 691;
Best Local Similarity 99.0%; Pred. No. 1.2e-91;
Matches 408; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

182 GCGACGTCCTCCCTCTCCACCCCGCGCGCGCCATAGACACAGAGCCGACA 241
2 GCGACGTCCTCCCTCTCCACCCCGCGCGCGCCATAGACACAGAGCCGACA 61
242 GCTAGATCGCGAAATCAGATATGGTGGCGGCAAGTGCAGCTGAACGATAGAGAC 301
62 GCTAGATCGCGAAATCAGG--ATGGGTGGCGGCAAGTGCAGCTGAACGATAGAGAC 119
302 AAGATAAATCGCGAGTGAACCTTCTCCAAAGCGCGCAAGGCTCTTAAGAGCGGAC 361
120 AAGATAAATCGCGAGTGAACCTTCTCCAAAGCGCGCAAGGCTCTTAAGAGCGGAC 179
362 GAGATCTCCGCTCTGTGAGCGGAGGTGCGCGTCACTGCTTCTCCCGCAAGGCGAC 421
180 GAGATCTCCGCTCTGTGAGCGGAGGTGCGCGTCACTGCTTCTCCCGCAAGGCGAC 239
422 CTATATAGTAGCGCACCGACTCCAGATGAGCAAAATCTTGAACGTTATGAGCGCTAC 481
240 CTATATAGTAGCGCACCGACTCCAGATGAGCAAAATCTTGAACGTTATGAGCGCTAC 299
482 TCTTATGTGAAAAGGCTTTATTTACGCTGAATCTGAAGTGAAGGAAATTTGGTCCAC 541
300 TCTTATGTGAAAAGGCTTTATTTACGCTGAATCTGAAGTGAAGGAAATTTGGTCCAC 359
542 GAATACAGGAACCTTAAGCGAAGATTGAGACCATACAAAATGTCAAGC 593
360 GAATACAGGAACCTTAAGCGAAGATTGAGACCATACAAAATGTCAAGC 411

LOCUS B212134 694 bp mRNA linear EST 04-APR-2002
DEFINITION B212134 Y. Ogihara unpublished cDNA library, Wh Triticum aestivum
CDNA clone wh34p04 5', mRNA sequence.
B212134
B212134
B212134.1 GI:19951373
EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
/ Trilicaceae; Triticum.
1 (bases 1 to 694)
Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished (2002)
Contact: Tadasi Shin-I
Center For Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES

source

Location/Qualifiers

1..694
/organism="Triticum aestivum"
/cultur="Chinese Spring"
/db_xref="taxon:4565"
/clone="wh34p04"
/clone_1b="Y. Ogihara unpublished cDNA library, Wh"
/tissue_type="spike at meiosis"
/dev_stage="Feekes' scale 9"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J. Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give plasmid phagemids in the T7 Close Lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."

BASE COUNT 211 a 181 c 189 g 113 t
ORIGIN

Query Match 66.6%; Score 394.8; DB 13; Length 694;
Best Local Similarity 99.0%; Pred. No. 1.2e-91;
Matches 408; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

182 GCGACGTCCTCCCTCTCCACCCCGCGCGCGCCATAGACACAGAGCCGACA 241
2 GCGACGTCCTCCCTCTCCACCCCGCGCGCGCCATAGACACAGAGCCGACA 61
242 GCTAGATCGCGAAATCAGATATGGTGGCGGCAAGTGCAGCTGAACGATAGAGAC 301
62 GCTAGATCGCGAAATCAGG--ATGGGTGGCGGCAAGTGCAGCTGAACGATAGAGAC 119
302 AAGATAAATCGCGAGTGAACCTTCTCCAAAGCGCGCAAGGCTCTTAAGAGCGGAC 361
120 AAGATAAATCGCGAGTGAACCTTCTCCAAAGCGCGCAAGGCTCTTAAGAGCGGAC 179
362 GAGATCTCCGCTCTGTGAGCGGAGGTGCGCGTCACTGCTTCTCCCGCAAGGCGAC 421
180 GAGATCTCCGCTCTGTGAGCGGAGGTGCGCGTCACTGCTTCTCCCGCAAGGCGAC 239
422 CTATATAGTAGCGCACCGACTCCAGATGAGCAAAATCTTGAACGTTATGAGCGCTAC 481
240 CTATATAGTAGCGCACCGACTCCAGATGAGCAAAATCTTGAACGTTATGAGCGCTAC 299
482 TCTTATGTGAAAAGGCTTTATTTACGCTGAATCTGAAGTGAAGGAAATTTGGTCCAC 541
300 TCTTATGTGAAAAGGCTTTATTTACGCTGAATCTGAAGTGAAGGAAATTTGGTCCAC 359
542 GAATACAGGAACCTTAAGCGAAGATTGAGACCATACAAAATGTCAAGC 593
360 GAATACAGGAACCTTAAGCGAAGATTGAGACCATACAAAATGTCAAGC 411

LOCUS B1956235 1196 bp mRNA linear EST 22-OCT-2001
DEFINITION B1956235 Hordeum vulgare rachis EST library HVCDNA0015
(normal) Hordeum vulgare cDNA clone HVSMEN001F21f, mRNA sequence.
B1956235
B1956235
B1956235.1 GI:16306797
EST.
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
/ Trilicaceae; Hordeum.
1 (bases 1 to 1196)
Wang, R., Close, T.J., Kleinhofs, A., Wise, R., Chin, A., Begum, D.,

FRISCH, D., ATKINS, M., YU, Y., HENRY, D., PALMER, M., RAMBO, T., SIMMONS, J., OATES, R. and MAIN, D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex rachis cDNA library
Unpublished (2001)
Contact: Wing RA

Friesch, D., Atkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simonson, J., Oates, R. and Main, D.,
Development of a genetically and physically anchored EST resource
for barley genomics: Morex rachis cDNA library
Unpublished (2001)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu
Total hg bases = 172
Seq primer: AATTAACCCCTCACAAGG
High quality sequence start: 3
High quality sequence stop: 1100.

FEATURES	Location/Qualifiers
source	1. .1196

/organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HUSMEN0001P21f"
 /clone_lib="Hordeum vulgare rachis EST library HVCNDA0015
 (normal)"
 /tissue_type="Rachis"
 /lab_host="TJ0121"
 /note="Vector: pluscript SK(-); Site 1: EcoRI; Site 2:
 XhoI; Plants were grown at Washington State University,
 Pullman, WA in a greenhouse, the rachises were excised and
 frozen in liquid nitrogen (Kleinofsky lab). In the TJC close
 lab at the University of California, Riverside total RNA
 was prepared, poly(A) was purified, one primary
 unamplified cDNA library was made, and 1 million plv were
 in vivo excised to give pluscript SK(-) cDNA phagmids
 (Chn). Phagmids were plated and picked at the Clemson
 University Genomics Institute (CUGI) (Begum, Palmer,
 Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
 sequencing and sequence analysis were performed at CUGI
 (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The
 sequence has been trimmed to remove vector sequence and
 contains a minimum of 100 bases of phred value 20 or
 above. For more details on library preparation and
 sequence analysis see
<http://www.genome.clemson.edu/projects/barley>. To order
 this clone see <http://www.genome.clemson.edu/orders> Also
 see Close TJ, Wing R, Kleinofsky A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. *Barley Genetics Newsletter* 31:29-30
 (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"

BASE COUNT	278 a	439 c	270 g	172 t.	37 others
ORIGIN					

	Query Match	Similarity	65.1%	Score 386	DB 13	Length 1196
	Best Local	Similarity	94.5%	Pred. No. 2.7e-89		
	Matches	410	Conservative	0	Mismatches 22	Indels 2
					Gaps	1
Oy	160	CCCTCACC	CGCGCGGACGACGAGCTCTGCTCTCTCCACCCCGCGCGCTGCGC	219		
Db	1	CCCTCACC	CGCGCGGACGACGAGCTCTGCTCTCTCCACCCCGCGCGCTGCGC	60		
Oy	220	GCCATAGA	CAACAAGCGCCGACGACTAGATCGCGGAATCAGATATAGGGTCGGGGCAAGGT	279		
Db	61	GCCATANG	CACACGACGCCGACCTTAGAGGGTGGAAATCGGG--ATGGGTGCGCGTAGGT	118		
Oy	280	GCAAGTGA	ACCGGATAGAGAACAGATAAATCGGACGGTGCACCTTCTCCAAAGCGCGCAA	339		
Db	119	GCANTCTGA	ACCGGATAGAGAACAGATAAATCGGACGGTGCACCTTCTCCAAAGCGCGCAA	178		
Oy	340	CGGGCTCT	CGAAGAAAGGCGACAGAGTCTCCGTCCTCTGTGACGGGGAGGTGCGCGTAT	399		
Db	179	CGGGCTCT	CGAAGAAAGGCGACAGAGTCTCCGTCCTCTGTGACGGAGGTGCGCGTAT	238		
Oy	400	GCTCTCTT	CCCCAAGGCAAGCTCTATGATGATGCGCACCGACTCCAGCATGAGACAAAT	459		

Db 239 CGTCTTCTCCCCAAAGCGAAGCTGTATGAGTAAAGCCACCGACTCCAGATGAGCAAAAT 298

QY 460 TCTTGAACGTTATGAGCGCTACTTTATGCTGAAAAAGCTCTTATTTGACTGAATCTGA 519

Db 299 TCTTGAACGTTATGAGCGCTACTTTATGCTGAAAAAGCTCTTATTTGACTGAATCTGA 358

QY 520 AAGTAGGGAATTTGGTGCACGAATACAGAAACTTAAAGCGAAGATTGAGACCATACA 579

Db 359 AAGTAGGGAATTTGGTGTCTATGAATACAGAAACTTAAAGCGAAGATTGAGACCATCA 418

QY 580 AAAATGTCACAAGC 593

Db 419 GAAGTGGCAACAAGC 432

RESULT 9	Bj213269	658 bp	mRNA	linear	EST 04-APR-2002
LOCUS	Bj213269				
DEFINITION	Bj213269	Y. Ogihara unpublished cDNA library, Wh	Triticum aestivum		
ACCESSION	Bj213269	cdna clone wh2132 5', mRNA sequence.			
VERSION	Bj213269.1	GI:19952768			
KEYWORDS	EST.				
SOURCE	bread wheat.				
ORGANISM	Triticum aestivum				

REFERENCE	1 (pages 1 to 658)
AUTHORS	Ogihara, Y. and Murai, K.
TITLE	Expressed genes in <i>Triticum aestivum</i>
JOURNAL	Unpublished (2002)
COMMENT	Contact: Tadasu Shin-i

Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshint@genes.nig.ac.jp.

FEATURES	Location/Qualifiers
source	1. .658

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/organism="Trilicium aestivum"
/cultivar="Chinese Spring"
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/clone="wh2152"
/clone_1b="Y. Ogihara unpublished cDNA library, wh"
/tissue_type="spike at meiosis"
/dev_stage="Feekes' scale 9"
/notes="Vector: Lambda Uni-ZAP XR, excised phagemid:
Site_1: EcoRI, Site_2: XhoI; plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pluescript phagemids in the Yu Close lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA
sequencing were
performed in the OD Anderson lab (all other authors). "

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Query Match	99.0%	Score 385.4	DB 13	Length 658
Best Local Similarity	95.0%	Pred. No. 3.2e-89		
Matches	409	Conservative	0	Mismatches 1
			Indels	3
			Gaps	2
QY	182	GGAGAGTCTCGCCCTCTCTCCACCCCGCGCGCGCGCGCGCGCATATG-ACACAAAGCCAC	240	
Db	6	GGAGAGTCTCGCCCTCTCTCCACCCCGCGCGCGCGCGCGCATATGATACACAAAGCCAC	65	

OY 241 AGCTGATCGGAAATCGATATGGTTCGCGCAGGTGCACTGAAAGCGATGAGAA 300
 |||||||
 DB 66 AGTAGATCGGAAATCAGG--ATGGTTCGCGCAAGGTGACGTGAAGCGGATGAGAA 123
 |||||||
 OY 301 CAAGTAATCGGAGGAGACCTCTCGAAGGCGCGCAAGGCGCTCGAAGAAAGCGCA 360
 |||||||
 DB 124 CAAGTAATCGGAGGAGACCTCTCGAAGGCGCGCAAGGCGCTCGAAGAAAGCGCA 183
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 OY 361 CGAGATCTCGCTCTCTGTGACGCGGAGAGCGCGCTCATGCTCTTCCCCCAAGGCA 420
 184 CGAGATCTCGCTCTCTGTGACGCGGAGAGCGCGCTCATGCTCTTCCCCCAAGGCA 243
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 OY 421 GCTCTATGATGACCGCACCGACCTCAGCATGGAACAAATTTCTTAAGCTTATGACGCTA 480
 244 GCTCTATGATGACCGCACCGACCTCAGCATGGAACAAATTTCTTAAGCTTATGACGCTA 303
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 |||||||
 OY 304 CTCTATGCTGAAAAGGCTCTTATTTAGCTGAATCTGAAGTGGGAATTTGTGCA 363
 |||||||
 DB 541 CGAATACGAGAACTTAAGCGAAGATTGAGACCATACAAATATGTCAAGC 593
 364 CGAATACGAGAACTTAAGCGAAGATTGAGACCATACAAATATGTCAAGC 416
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RESULT 10
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 LOCUS
 DEFINITION
 WHE0964_G04_M0825 wheat pre-anthesis spike cDNA library Triticum
 aestivum cDNA clone WHE0964_G04_M08, mRNA sequence.
 BE498620
 BE498620.1 GI:9697237
 EST.

SOURCE

bread wheat.
Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
 ; Triticeae; Triticum.
 1 (bases 1 to 551)

REFERENCE

Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han,

AUTHORS

P.S., Hsia, C.C., Kang, Y., Iazo, G.R., Miller, R., Rausch, C.J.,
Seaton, C.U., and Tong, J.C.

TITLE

The structure and function of the expressed portion of the wheat
genomes - Pre-anthesis spike cDNA library

JOURNAL

Unpublished (2000)

COMMENT

Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818

FEATURES

Source
Email: oanderson@usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: StrataGene SK primer.

FEATURES

Location/Qualifiers
1..551

SOURCE

1..551
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/clone_lib="wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI, Site 2: XhoI; plants were grown in the
greenhouse. Whole spike with awns trimmed, white, green
and yellow anther were collected and total RNA, and
poly(A) RNA were prepared, a cDNA library was made, and
the cDNA clones were in vivo excised to give plasmid
phagemids in the TJ Close Lab (Choi, Close, Fenton) at
the University of California, Riverside. Plasmid DNA

BASE COUNT 162 a 141 c 143 g 105 t
 ORIGIN
 preparations and DNA sequencing were performed in the OD
 Anderson lab (all other authors)."
 Query Match 64.8%; Score 384.4; DB 10; Length 551;
 Best Local Similarity 99.2%; Pred. No. 5.5e-89;
 Matches 397; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

OY 194 CTCTCCACCCCGCGCGCGCGCGCATAGACAGAGCGGACAGCTAGATCGGA 253
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 DB 1 CTCTCCACCCCGCGCGCGCGCGCATAGACAGAGCGGACAGCTAGATCGGA 60
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 OY 254 AATCAGATATGAGTCCGCGGCAAGTCCAGTGAAGCGGATAGAAACAATATTCG 313
 61 AATCAGG--ATGGTCCGCGGCAAGTCCAGTGAAGCGGATAGAAACAATATTCG 118
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 OY 374 CTCTGACGCGGAGGTGCGCGTATGCTCTTCCCAAGGCGCAAGATCTAGATAC 433
 179 CTCTGACGCGGAGGTGCGCGTATGCTCTTCCCAAGGCGCAAGATCTAGATAC 238
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 OY 434 GCCACGACTTCACATGACAAATCTTGAACGTATGAGCGCTACTTATGCTGAA 493
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 |||||||
 OY 494 AAGGCTCTTATTTAGCTGAATCTGAAGTGAAGGAATTTGTGCCAAGATACAGAAA 553
 299 AAGGCTCTTATTTAGCTGAATCTGAAGTGAAGGAATTTGTGCCAAGATACAGAAA 358
 |||||||
 DB 554 CTTAAGCGAAGATTGAGACCATCAAAATATGTCAAGC 593
 359 CTTAAGCGAAGATTGAGACCATCAAAATATGTCAAGC 398
 |||||||

REFERENCE

Wing, R., Close, T.J., Klein, A., Wise, R., Chin, A., Begum, D.,
Frisch, D., Atkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons,
J., Oates, R., and Main, D.

AUTHORS

Development of a genetically and physically anchored EST resource
for barley genomics: Morex rachis cDNA library

TITLE

Unpublished (2001)

JOURNAL

Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu

COMMENT

Total hg bases = 419
Seq primer: AATTAACCTCACAAGG
High quality sequence stop: 591.

FEATURES

Location/Qualifiers
1..622

SOURCE

1..622
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"

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(normal)"
/tissue_type="Rachis"
/lab_host="TJUC121"
/notes="vector: pBluescript SK(-); Site 1: EcoRI, Site 2:
XhoI; Plants were grown at Washington State University,
Pullman, WA in a greenhouse, the rachises were excised and
frozen in liquid nitrogen (Kleinbols lab). In the TJ Close
lab at the University of California, Riverside total RNA
was prepared, poly(A) was purified, one primary
unamplified cDNA library was made, and 1 million pfu were
in vivo excised to give pBluescript SK(-) cDNA phagemids
(Chin). Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Friesch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Friesch, Henry, Simmons, Rambo, Main). The
sequence has been trimmed to remove vector sequence and
contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinbols A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30
(http://wheat.pw.usda.gov/gspages/bgn/31/cover.html)"

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BASE COUNT      179 a      152 c      177 g      113 t
ORIGIN

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Query Match      60.8%; Score 360.8; DB 13; Length 622;
Best Local Similarity 94.1%; Pred. No. 7.3e-83;
Matches 386; Conservative 0; Mismatches 22; Indels 2; Gaps 1;

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OY 184 GACGTCCTGCTCTCTCCACCCCGCGCGCGCCATAGACACAGACCCGACAGC 243
DB 1 GACGGGGGGGGTGTCTCCACCTCCGCGCGCGCGCCATAGACACAGACCCGACAGC 60
OY 244 TAGATCGGGAATCAGATATGGTTCGGCGCAAGTGCAGTCCGATGAGAAACAA 303
DB 61 TAGATCGGGAATCAGATATGGTTCGGCGCAAGTGCAGTCCGATGAGAAACAA 118
OY 304 GATAATCGGCGAGTGACCTTCTCCAAAGCGCGCAAGGGCTCTGAAAGAAAGCGCACA 363
DB 119 GATAATCGGCGAGTGACCTTCTCCAAAGCGCGCAAGGGCTCTGAAAGAAAGCGCACA 178
OY 364 GATCTCCGCTCTGTGACGCGAGGTGCGCGCTCATCTCTTCTCCCGCAAGGCAAGCT 423
DB 179 GATCTCCGCTCTGTGACGCGAGGTGCGCGCTCATCTCTTCTCCCGCAAGGCAAGCT 238
OY 424 CTATAGTACGCGACCGAGCTCCAGCATGAGCAAAATTTCTTGAAGCTTATGAGCGTATC 483
DB 239 CTATAGTACGCGACCGAGCTCCAGCATGAGCAAAATTTCTTGAAGCTTATGAGCGTATC 298
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DB 299 TTATGCTGAAAAGGCTTATTTCACTGATCTGAAATGAGGGAATTTGTTGCGACA 358
OY 544 ATACAGAAAATTAAAGCGAGATTGAGACATACAAAATGTCACAAGC 593
DB 359 ATACAGAAAATTAAAGCGAGATTGAGACATACAAAATGTCACAAGC 408

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RESULT 12
BU211202      623 bp      mRNA      linear      EST 04-APR-2002
LOCUS        BU211202 Y. Ogihara unpublished cDNA library, Wh Triticum aestivum
DEFINITION   cDNA clone wh38g11.5, mRNA sequence.
ACCESSION    BU211202
VERSION      BU211202.1 GI:19950086
KEYWORDS     EST.
SOURCE       bread wheat.

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ORGANISM      Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
REFERENCE     1 (bases 1 to 623)
AUTHORS      Ogihara, Y. and Murai, K.
TITLE        Expressed genes in Triticum aestivum
JOURNAL      Unpublished (2002)
COMMENT      Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tahin@genes.nig.ac.jp.

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FEATURES
Source

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1. 623
/organism="Triticum aestivum"
/dev_stage="spike at meiosis"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="wh38g11"
/clone.lib="Y. Ogihara unpublished cDNA library, Wh"
/tissue_type="spike at meiosis"
/dev_stage="feeder" scale 9"
/notes="vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in U Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pBluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Kianin, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."

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BASE COUNT      195 a      158 c      165 g      102 t
ORIGIN

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Query Match      54.8%; Score 325; DB 13; Length 623;
Best Local Similarity 99.4%; Pred. No. 1.4e-73;
Matches 325; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 267 GTCCGGGCAAGTGCAGTGAAGCGGATAGAGCAAGATTAATCGCAGGTGACTTCT 326
DB 1 GTCCGGGCAAGTGCAGTGAAGCGGATAGAGCAAGATTAATCGCAGGTGACTTCT 60
OY 327 CCAAGCGCGCAAGGGCTCTGAAAGAGCGCAGAGATCTCCGTCTGTGACGGCG 386
DB 61 CCANNCGCGCAAGGGCTCTGAAAGAGCGCAGAGATCTCCGTCTGTGACGGCG 120
OY 387 AGTGCGCGTATGCTCTTCTCCCGCAAGGCAAGCTTATGAGTAGCCAGCTTCA 446
DB 121 AGTGCGCGTATGCTCTTCTCCCGCAAGGCAAGCTTATGAGTAGCCAGCTTCA 180
OY 447 GCATGGAACAATTTGGAAGCTTATGAGGCTACTCTTATGCTGAAAGGCTCTTATT 506
DB 181 GCATGGAACAATTTGGAAGCTTATGAGGCTACTCTTATGCTGAAAGGCTCTTATT 240
OY 507 CAGCTGATCTGAAAGTGAGGAAATTGTTGCCAGATACAGAACTTAAGCGGAGA 566
DB 241 CAGCTGATCTGAAAGTGAGGAAATTGTTGCCAGATACAGAACTTAAGCGGAGA 300
OY 567 TTGAGACCATACAAAATGTCACAAGC 593
DB 301 TTGAGACCATACAAAATGTCACAAGC 327

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RESULT 13
BQ778659      572 bp      mRNA      linear      EST 26-JUL-2002
LOCUS        BQ778659
DEFINITION   94613A11.y1 946 - tassell primordium prepared by Schmidt lab 2ea

```

ACCESSION mays cDNA, mRNA sequence.
 VERSION B0778659
 KEYWORDS B0778659.1 GI:21987131
 SOURCE EST.
 ORGANISM Zea mays.

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 572)

AUTHORS Maize ESTs from various cDNA libraries sequenced at Stanford
 TITLE University

JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 94613 row: A column: 11.

FEATURES
 SOURCE location/Qualifiers
 1..572
 /organism="Zea mays"
 /cultivar="OH43"
 /db_xref="taxon:4577"
 /clone_lib="946 - tassels primordium prepared by Schmidt
 lab"
 /tissue_type="tassels"
 /dev_stage="just after the transition from vegetative to
 inflorescence development"
 /lab_host="X10LR"
 /note="Organ: tassels; Vector: Hybrizap; Site_1: Ecor1;
 Site_2: Xho1; George Chuck dissected immature tassels
 between 1mm and 3mm. Sharon Stanfield prepared the cDNA
 library in Hybrizap. Sample insert size range was 350 bp
 to 3 kb with a 1 kb average."
 148 a 179 c 147 g 98 t

BASE COUNT
 ORIGIN

Query Match 51.3%; Score 304; DB 14; Length 572;
 Best Local Similarity 79.2%; Pred. No. 3.6e-68;
 Matches 374; Conservative 0; Mismatches 95; Indels 3; Gaps 1;

122 CCTTCTCTCCCATCTTAAGTGCATCCATCTCCCTCACCGCGCGGCGACCA 181
 50 CTTCCCGATCCCTCTTCACTCACTCACTCTTTAAAGCTAACCGACTACCTGCT 109
 182 GCGACGTCGCTCTCTCCACCCCGCGCGGCGGCGCATAGACACAGAGCCGACA 241
 110 GCGTCGCTCAACTCGCGCGCGCGCGGCGGCGCATACCGGAGAGAGAGAGAGCA 169
 242 GCTAGATCGCAAAATCAGATATGGGTGGCGCAAGGTGCACTTAAAGGATAGAGAC 301
 170 GATCG---GAGGCGAGCGAAGATGGGGCGCGCAAGGTGCAAGCGATAGAGAAC 226
 302 AAGATTAATGGCGAGGTGACCTTCTCCAGCGCGCAACGGGGCTCTTAAGAGCGGAC 361
 227 AAGATTAACCGGAGCGGACCTTCTCCAGCGCGGAAAGGGGCTGCTAAAGAGCGGAC 286
 362 GAGATCTCCGCTCTGTGACGCGGAGGTGCGCGCATGCTTCTCCCGCAAGAGGCAAG 421
 287 GAGATCTCCGCTCTGTGACGCGGAGGTGCGCGCATGCTTCTCCCGCAAGAGGCAAG 346
 422 CTATATGAGTACCGCAGCTCCAGATGAGCAAAATTTCTGAACGTTATGAGGCGTAC 481
 347 CTATACGAGTACCGCTCCAGCTCCCGCATGAGCAAAATTTCTGAACGTTATGAGGATAT 406
 482 TCTATATGAGTACCGCTCTTATTCAGCTGAATCTGAATGAGGAGAAATTTGGTGCAC 541
 407 TCTATATGAGTACCGCTCTTATTCAGCTGAATCTGAATGAGGAGAAATTTGGTGCAC 466

542 GAATACAGAAACTTAAGCGAGATGAGACCATACCAAAATGTCACACAC 593
 467 GAATACAGAAACTTAAGCGAGATGAGACCATACCAAAATGTCACACAC 518

RESULT 14
 LOCUS AY109845
 DEFINITION Zea mays CL2300_1 mRNA sequence.
 ACCESSION AY109845
 VERSION AY109845.1 GI:21213723
 KEYWORDS HTC.
 SOURCE Zea mays.

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 1488)

REFERENCE Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whiteside,M.S.,
 Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
 Maize Mapping Project/Dupont Consensus Sequences for Design of
 Overgo Probes

AUTHORS

TITLE Unpublished (2002)
 2 (bases 1 to 1488)

JOURNAL

REFERENCE Direct Submission
 Submitted (25-APR-2002) Maize Mapping Project, University of
 Missouri, Columbia, MO 65211, USA

FEATURES
 SOURCE location/Qualifiers
 1..1488
 /organism="Zea mays"
 /db_xref="maizedb:630908"
 /db_xref="taxon:4577"
 /clone_lib="CL2300_1"
 /note="this sequence is part of a project of EST
 assemblies resulting from the application of public
 contigs to seed Dupont contigs; this resource was
 assembled by Dupont as part of a collaboration for the
 overgo addressing of BACs in conjunction with the Maize
 Mapping Project"

BASE COUNT 285 a 288 c 292 g 238 t 385 others
 ORIGIN

Query Match 49.0%; Score 290.4; DB 11; Length 1488;
 Best Local Similarity 89.5%; Pred. No. 1.6e-64;
 Matches 306; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

252 GAATACAGATATGAGTGGCGGCAAGGTGAGCGGATGAGCAAAATGTAATC 311
 138 GCAACAAAGGCGATGGGCGCGGCAAGGTACGCTGAAGCGGATGAGCAAAATGTAATC 197
 312 GCGAGTACCTTCTCCAGGCGCGCAAGGCTCTGAAAGAGAGCGCAGATCTCCG 371
 198 GCGAGTACCTTCTCCAGGCGCGCAAGGCTCTGAAAGAGAGCGCAGATCTCCG 257
 372 TCTCTGTGACGCGGAGGTGCGGCTCATGCTTCTCTCCCAAGGCAAGCTTATGAGT 431
 258 TCTCTGTGACGCGGAGGTGCGGCTCATGCTTCTCTCTNNNNNAAGGCAAGCTTACGAGT 317
 432 ACGGCGAGCTCCGAGATGAGCAAAATTTCTGAAAGCTTATGAGCGCTATGAGT 491
 318 ACGGCGAGCTCCGAGATGAGCAAAATTTCTGAAAGCTTATGAGCGCTATGAGT 377
 492 AAAAGCTCTTATTTAGCTGAATCTGAAAGTGAAGGAAATTTGTTGCGCAGATACAGA 551
 378 AAAAGCTCTTATTTAGCTGAATCTGAAAGTGAAGGAAATTTGTTGCGCAGATACAGA 437
 552 AACTTAAGCGAGATGAGCAATACCAAAATGTCACAGC 593
 438 AACTTAAGCGAGATGAGCAATACCAAAATGTCACAGC 479

AC Q9W7C6.
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE FDMADS6.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eubharidiales; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GUNGUAI 4;
RL Jia H., Cong B., Shao J., Sun C.;
RA Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; AF139664; AAF66997.2; -.
DR HSSP; P11831; 1SR5.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00404; MADS_DOMAIN.
DR SMART; SM00432; MADS_1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 246 AA; 28394 MW; DE0391D606D9B83B CRC64;

Alignment Scores:
Pred. No.: 2,456-37 Length: 246
Score: 505.00 Matches: 96
Percent Similarity: 95.45% Conservative: 9
Best Local Similarity: 87.27% Mismatches: 5
Query Match: 49.03% Indels: 0
DB: Gaps: 0

US-10-020-338-8 (1-593) x Q9W7C6 (1-246)

QY 263 ATGGGTGCGGCAAGGTGACGTGAGGAGTATGAGCAAGATTAATCGCAGGTGACC 322
DB 1 MetGlyArgGlyLysValGlnLeuLysArgIleGlnuAnThrIleAsnArgGlnValThr 20
QY 323 TTCTTCAAGCGCGCAAGCGGCTCTGGAAGAGCGCAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgSerGlyLeuLeuLysLysAlaGlnIleSerValLeuLysAsp 40
DB 383 GCGGAGTGCCTGATGCTCTTCTCCCAAGGCAAGCTCTATGATGACCGCAC 442
DB 41 AlaGlnValAlaIleLeuIlePheSerThrLysGlyLysLeuLysLysValAlaThrAsp 60
QY 443 TCCAGCATGAGCAAAATTTCTTGAAGCTATGAGCGCTCTCTATGCTGAAAAGGCTTT 502
DB 61 SerCysMetAspLysIleLeuGlnArgGlyGlnuArgLysSerLysAlaGlnLysValLeu 80
QY 503 ATTTCAGTGAATCTGAAGTGAAGGGAATGTGTCGACGATACAGAACTTAAGCGG 562
DB 81 IleSerAlaGlnuSerAspThrGlnLysAnThrCysHisGlnLysGlnLysValAla 100
QY 563 AAGATTGAGACCATACAAAATGTCAACAG 592
DB 101 LysValGlnuThrIleGlnLysCysGlnLys 110

RESULT 13

082128 PRELIMINARY; PRT; 244 AA.
ID 082128;
AC 082128;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE MADS box transcription factor.
GN TAMADS#11.

OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA Murai K., Murai R., Takumi S., Ogihara Y.;
RT "CDNA cloning of three MADS box genes in wheat (Accession Nos.
RT AB007504, AB007505 and AB007506) (PCR98-159).";
RL Plant Physiol. 118:330-330 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Murai K., Murai R., Takumi S., Ogihara Y.;
RT "Cloning and characterization of cDNAs corresponding to the wheat MADS
RT box genes.";
RL (In) Slinkard A.E. (eds.);
RL Proceedings of the 9th International Wheat Genetics Symposium.
RL pp.89-94, University Extension Press, Saskatchewan, Canada (1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; AB007504; BA033457.1; -.
DR HSSP; P11746; 1MM.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADS_DOMAIN.
DR SMART; SM00432; MADS_1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 244 AA; 27718 MW; SEE86E9A4B75124B CRC64;

Alignment Scores:
Pred. No.: 3,726-37 Length: 244
Score: 503.00 Matches: 94
Percent Similarity: 94.55% Conservative: 10
Best Local Similarity: 85.45% Mismatches: 6
Query Match: 48.83% Indels: 0
DB: Gaps: 0

US-10-020-338-8 (1-593) x 082128 (1-244)

QY 263 ATGGGTGCGGCAAGGTGACGTGAGGAGTATGAGCAAGATTAATCGCAGGTGACC 322
DB 1 MetGlyArgGlyLysValGlnLeuLysArgIleGlnuAnThrIleAsnArgGlnValThr 20
QY 323 TTCTTCAAGCGCGCAAGCGGCTCTGGAAGAGCGCAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgSerGlyLeuLeuLysLysAlaGlnIleSerValLeuLysAsp 40
QY 383 GCGGAGTGCCTGATGCTCTTCTCCCAAGGCAAGCTCTATGATGACCGCAC 442
DB 41 AlaGlnValAlaIleLeuIlePheSerThrLysGlyLysLeuLysLysValAlaThrAsp 60
QY 443 TCCAGCATGAGCAAAATTTCTTGAAGCTATGAGCGCTCTCTATGCTGAAAAGGCTTT 502
DB 61 SerCysMetAspLysIleLeuGlnArgGlyGlnuArgLysSerLysAlaGlnLysValLeu 80
QY 503 ATTTCAGTGAATCTGAAGTGAAGGGAATGTGTCGACGATACAGAACTTAAGCGG 562
DB 81 ValSerSerGlnuSerGlnIleGlnLysAnThrCysHisGlnLysGlnLysValAla 100
QY 563 AAGATTGAGACCATACAAAATGTCAACAG 592
DB 101 LysValGlnuThrIleGlnLysCysGlnLys 110

RESULT 14

09LE12 PRELIMINARY; PRT; 244 AA.
ID 09LE12;
AC 09LE12;
DT 01-OCT-2000 (Tremblrel. 15, Created)

OY 563 AAGATTGACCATACAAAATGTCACAG 592
Db 101 LysValGluThrIleGlnLysCysGlnLys 110

RESULT 10

O9ZTT7 PRELIMINARY; PRT; 245 AA.

AC O9ZTT7;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE MADS-box protein 1.
GN MADS1.
OS Lolium temulentum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Poaceae; Lolium.
NCBI_TaxID=34176;
[1]
SEQUENCE FROM N.A.
RC STAIN=CERES;
RA Gocal G.F.W., Blundell C., Schwartz O.M., King R.W.;
RT "Expression of Two APERLAI-Related Genes Changes During Inflorescence
Initiation of Lolium.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF035378; AAD10625.1; -
DR HSSP; P11831; 1SRS.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 245 AA; 28039 MW; 5C4BEF15903ACC39 CRC64;

Alignment Scores:

Pred. No.: 1,62e-37 Length: 245
Score: 507.00 Matches: 96
Percent Similarity: 93.64% Conservative: 7
Best Local Similarity: 87.27% Mismatches: 7
Query Match: 49.22% Indels: 0
Gaps: 0

US-10-020-338-8 (1-593) x O9ZTT7 (1-245)

OY 263 ATGGTGGCGGCAAGTGCAGCTGAAGCGGATAGAGAACAGATAAATCGGACGTGAC 322
Db 1 MetGlyArgGlyLysValGlnLeuLysArgIleGlnLysIleAsnArgGlnValThr 20
OY 323 TTCTCCAAAGCGCGCAAGCGGCTCTGAAGAGCGGCGAGATCTCGTCTCTGTAC 382
Db 21 PheSerLysArgArgSerLysLeuLysLysAlaHisGlnLysSerValLeuLysAsp 40
OY 383 GCGAGGTGCGCGCATGCTTCTCCCGCAAGGCAAGCTTATGATGACCCACCGAC 442
Db 41 AlaGlnValAlaLeuLysIlePheSerThrLysGlyLysLeuLysGlnPheLysThrAsp 60
OY 443 TCCAGCATGACAAAATTTCTTAAGCGTTATAGCGGCTTATGCTGAAGAGCTCTT 502
Db 61 SerCysMetAspLysIleLeuGlnArgLysGlyArgLysSerValAlaGlnLysValLeu 80
OY 503 ATTTCAGTGAATCTGAAGAGGAAATTTGTCGACGATACAGAACTTAAGGCG 562
Db 81 IleSerThrGlnSerGlnLysGlnGlnLysAsnTrpCysHisGlnLysValLysAla 100
OY 563 AAGATTGACCATACAAAATGTCACAG 592
Db 101 LysValGluThrIleGlnLysCysGlnLys 110

Db 101 LysValGluThrIleGlnArgCysGlnLys 110

RESULT 11

O9SEXO PRELIMINARY; PRT; 246 AA.

AC O9SEXO;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE MADS14 protein.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eubartioideae; Oryzaceae; Oryza.
NCBI_TaxID=4530;
[1]
SEQUENCE FROM N.A.
RC TISSUE=FLOWER;
RA MEDLINE=99373407; PubMed=10444103;
RX Moon Y.H., Kang H.G., Jung J.Y., Jeon J.S., Sung S.K., An G.;
RT "Determination of the motif responsible for interaction between the
rice APERLAI/AGAMOUS-LIKE9 family proteins using a yeast two-hybrid
system.";
RL Plant Physiol. 120:1193-1204(1999).
DR EMBL; AF058697; AAF19047.1; -
DR HSSP; P11831; 1SRS.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; UNKNOWN_1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
SQ SEQUENCE 246 AA; 28523 MW; 3044628F2840AC53 CRC64;

Alignment Scores:

Pred. No.: 1,62e-37 Length: 246
Score: 507.00 Matches: 97
Percent Similarity: 95.45% Conservative: 8
Best Local Similarity: 88.18% Mismatches: 5
Query Match: 49.22% Indels: 0
Gaps: 0

US-10-020-338-8 (1-593) x O9SEXO (1-246)

OY 263 ATGGTGGCGGCAAGTGCAGCTGAAGCGGATAGAGAACAGATAAATCGGACGTGAC 322
Db 1 MetGlyArgGlyLysValGlnLeuLysArgIleGlnLysIleAsnArgGlnValThr 20
OY 323 TTCTCCAAAGCGCGCAAGCGGCTCTGAAGAGCGGCGAGATCTCGTCTCTGTAC 382
Db 21 PheSerLysArgArgSerLysLeuLysLysAlaHisGlnLysSerValLeuLysAsp 40
OY 383 GCGAGGTGCGCGCATGCTTCTCCCGCAAGGCAAGCTTATGATGACCCACCGAC 442
Db 41 AlaGlnValAlaLeuLysIlePheSerThrLysGlyLysLeuLysGlnPheLysThrAsp 60
OY 443 TCCAGCATGACAAAATTTCTTAAGCGTTATAGCGGCTTATGCTGAAGAGCTCTT 502
Db 61 SerCysMetAspLysIleLeuGlnArgLysGlyArgLysSerValAlaGlnLysValLeu 80
OY 503 ATTTCAGTGAATCTGAAGAGGAAATTTGTCGACGATACAGAACTTAAGGCG 562
Db 81 IleSerThrGlnSerGlnLysGlnGlnLysAsnTrpCysHisGlnLysValLysAla 100
OY 563 AAGATTGACCATACAAAATGTCACAG 592
Db 101 LysValGluThrIleGlnLysCysGlnLys 110
RESULT 12
O9M7C6 PRELIMINARY; PRT; 246 AA.

Db 41 AlaGluValAlaAlaIleValPheSerProLysGlyLysLeuTyrGluTyrAlaThrAsp 60

Qy 443 TCAGCATGACAAATTTCTGAACGTTATGAGCCGCTACTTATGCTGAAGAGCTCTT 502

Db 61 SerArgMetAspLysIleLeuGluLysArgTyrGluLysArgTyrSerTyrAlaGluLysAlaLeu 80

Qy 503 ATTTGAGCTGAATCTGAAGAGGGAATTTGCTCCAGCATATACAGAACTTAAAGCG 562

Db 81 IleSerAlaGluSerGluSerGluLysArgTyrGluLysArgTyrSerTyrAlaGluLysAlaLeu 100

Qy 563 AAGATTGAGACCATACAAATATGTCACAG 592

Db 101 LysIleGluThrIleGlnLysCysHisLys 110

RESULT 8

ID 004068 PRELIMINARY; PRT: 228 AA.

AC 004068:

DT 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

OC MADS box protein (Fragment).

OS Sorghum bicolor (Sorghum) (Sorghum vulgare).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;

OC Panicoideae; Andropogoneae; Sorghum.

OX NCBI_TaxID=4558;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=97218034; PubMed=9065695;

RA Greco R., Stegi L., Colombo L., Angenent G.C., Sari-Gorla M., Pe M.E.;

RT "MADS box genes expressed in developing inflorescences of rice and sorghum."

RL Mol. Gen. Genet. 253:615-623 (1997).

DR EMBL: U32110; AAB50181.1; -.

DR HSSP: P11831; ISRS.

DR TRANSFAC: T03172; -.

DR InterPro: IPR002487; TF_Kbox.

DR InterPro: IPR002100; TF_MADSbox.

DR Pfam: PF01486; K-box; 1.

DR Pfam: PF00319; SRF-TF; 1.

DR PRINTS: PR00404; MADS; 1.

DR SMART: SM00432; MADS; 1.

DR PROSITE: PS50066; MADS_BOX_2; 1.

DR NON TER 1

FT SEQUENCE 228 AA; 25999 MW; 3F70A30B6E23CC25 CRC64;

SO Alignment Scores:

Pred. No.: 2,036-40 Length: 228

Score: 539.00 Matches: 105

Percent Similarity: 99.06% Conservative: 0

Best Local Similarity: 99.06% Mismatches: 1

Query Match: 52.33% Indels: 0

DB: 10 Gaps: 0

US-10-020-338-8 (1-593) x 004068 (1-228)

Qy 275 AAGGTGCGCTGACGAGGTAGAGAAAGATTAATCGGAGGTGACTCTTCCAAAGCC 334

Db 1 LysValGlnLeuLysArgIleGlnLysIleAsnArgGlnValThrPheSerLysArg 20

Qy 335 CGCAACGGGCTCCCTGAAGAGCGACAGATCTCGCTCTGAGAGCGGAGGTGCGC 394

Db 21 ArgAsnGlyLeuLeuLysLysAlaHisGlnIleSerValLeuCysAspAlaGluValAla 40

Qy 395 GTCATGCTCTTCCCGCAAGAGCTATGAGTACGCGACCGCATCCAGCATGAGC 454

Db 41 ValIleValPheSerProLysGlyLysLeuTyrGluTyrAlaThrAspSerArgMetAsp 60

Qy 455 AAAATCTTTGAACGTTATGAGCGCTACTCTTATGCTGAAGAGCTCTTATTTACAGTAA 514

Db 61 LysIleLeuGluLysArgTyrGluLysArgTyrSerTyrAlaGluLysAlaLeuIleSerAlaGlu 80

Qy 515 TCTGAAGTGAAGGAAATTTGCTGCCAGCAATACAGAAACTTAAGCGGACATTGAGACC 574

Db 81 SerGluSerGluGlyAsnTyrCysHisGlnIlyrArgLysLeuLysAlaLysIleGluThr 100

Qy 575 ATACAAATATGTCACAG 592

Db 101 IleGlnLysCysHisLys 106

RESULT 9

ID 09MAY7 PRELIMINARY; PRT: 246 AA.

AC 09MAY7:

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE AP1-like MADS box protein.

GN RAP1B.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Euphorbiaceae; Oryzae; Oryza.

OX NCBI_TaxID=4530;

RN [1]

RP SEQUENCE FROM N.A.

RA Kyzuka J., Kobayashi T., Morita M., Shimamoto K.;

RT "Spatially and temporally regulated expression of rice MADS box genes with similarity to Arabidopsis class A, B, C genes."

RL Plant Cell Physiol. 0:0-0(2000).

CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.

DR EMBL: AB041020; BAA94342.1; -.

DR HSSP: P11831; ISRS.

DR InterPro: IPR002487; TF_Kbox.

DR InterPro: IPR002100; TF_MADSbox.

DR Pfam: PF01486; K-box; 1.

DR Pfam: PF00319; SRF-TF; 1.

DR PRINTS: PR00404; MADSDOMAIN.

DR SMART: SM00432; MADS; 1.

DR PROSITE: PS00350; MADS_BOX_1; 1.

DR PROSITE: PS50066; MADS_BOX_2; 1.

KW DNA-binding; Nuclear protein; Transcription regulation.

SO SEQUENCE 246 AA; 28489 MW; DF357FC94FB9B2FD CRC64;

Alignment Scores:

Pred. No.: 3,056-38 Length: 246

Score: 515.00 Matches: 98

Percent Similarity: 96.36% Conservative: 8

Best Local Similarity: 89.09% Mismatches: 4

Query Match: 50.00% Indels: 0

DB: 10 Gaps: 0

US-10-020-338-8 (1-593) x 09MAY7 (1-246)

Qy 263 ATGGGTGCGCGCAAGGTGACGCTGACGAGTACGAGAAAGATTAATCGGAGGTGACC 322

Db 1 MetGlyArgGlyLysValGlnLeuLysArgIleGlnLysIleAsnArgGlnValThr 20

Qy 323 TTCTCCAAAGCGCGCAAGGGCTCTGAAGAGCGACAGATCTCCGCTCTGTGAC 382

Db 21 PheSerLysArgArgSerGlyLeuLeuLysLysAlaHisGlnIleSerValLeuCysAsp 40

Qy 383 GCGAGGCGCGCGCATGCTCTTCCCGCAAGAGCTATGAGTACGCGACCGAC 442

Db 41 AlaGluValAlaLeuIleIlePheSerThrLysGlyLysLeuTyrGluTyrAlaThrAsp 60

Qy 443 TCAGCATGACAAATTTCTGAACGTTATGAGCGCTACTCTTATGCTGAAGAGCTCTT 502

Db 61 SerGlySerAspLysIleLeuGluLysArgTyrGluLysArgTyrSerTyrAlaGluLysValLeu 80

Qy 503 ATTTGAGTGAATCTGAAGAGTGAAGAAATTTGCTCCAGCATATACAGAACTTAAAGCGC 562

Db 81 IleSerAlaGluSerAspThrGlnGlnIlyAsnTyrCysHisGlnIlyrArgLysLeuLysAla 100

DB: 10 Gaps: 0
US-10-020-338-8 (1-593) x Q9FR84 (1-267)

QY 263 ATGGGTGCGGCAAGGTGACCTGAGCGGATAGAGAACAGATTAATCGCAGGTGACC 322
Db 1 MetGlyArgGlyValGlnLeuValArgIleGlnAsnValIleAsnArgGlnValThr 20
QY 323 TTCTCCAAAGCGCGCAACGGGCTCTGGAAGAGCGGACGAGATCTCGCTCTGTGAC 382
Db 21 PheSerLysArgGlnGlyLeuValGlnLeuValGlnLeuValGlnLeuValGlnLeuVal 40
QY 383 GCGAGAGTCCCGCATGCTCTTCTCCCGCAAGGCAAGCTATGATGATGACCGCAGC 442
Db 41 AlaeGluValAlaValIleValIleValIleValIleValIleValIleValIleValIleVal 60
QY 443 TCCAGCATGACCAAAATTTCTTGAACGTTATGAGCGCTACTTATGCTGAAAAGCTCTT 502
Db 61 SerArgMetAspLysIleLeuGlnArgGlyArgGlyArgGlyArgGlyArgGlyArgGlyArg 80
QY 503 ATTTCAGCTGAATCTGAAAGTGAAGGGAATTTGGTCCGCAAGTACAGAACTTAAGCG 562
Db 81 IleSerIleGlnSerGlnSerGlnSerGlnSerGlnSerGlnSerGlnSerGlnSerGlnSer 100
QY 563 AAGATTGAGACCATACAAAATGTCAACAG 592
Db 101 LysIleGlnThrIleGlnArgCysHisLys 110

RESULT 6

Q9FR84 PRELIMINARY; PRT; 270 AA.

ID Q9FR84
AC Q9FR84
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE MADS box protein 3.
GN MADS3.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A188;
RX MEDLINE=21437929, PubMed=11553732;
RA Heuer S., Hansen S., Bantlin J., Bretschneider R., Kranz E., Lorz H.,
Dresselhaus T.;
"The maize MADS box gene ZmMADS3 affects node number and spikelet
development and is co-expressed with ZmMADS1 during flower
development, in egg cells, and early embryogenesis";
RL Plant Physiol. 127:33-45(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL: AF112150; AAG43200.1; -
DR HSRP: P11831; 1SRP.
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF01486; K-box; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 270 AA; 31039 MW; 253CA21C3ED5B5FD CRC64;

Alignment Scores:
Pred. No.: 9.09e-42 Length: 270
Score: 554.00 Matches: 107
Percent Similarity: 99.09% Conservative: 2
Best Local Similarity: 97.27% Mismatches: 1
Query Match: 53.79% Indels: 0

DB: 10 Gaps: 0
US-10-020-338-8 (1-593) x Q9FR84 (1-270)

QY 263 ATGGGTGCGGCAAGGTGACCTGAGCGGATAGAGAACAGATTAATCGCAGGTGACC 322
Db 1 MetGlyArgGlyValGlnLeuValArgIleGlnAsnValIleAsnArgGlnValThr 20
QY 323 TTCTCCAAAGCGCGCAACGGGCTCTGGAAGAGCGGACGAGATCTCGCTCTGTGAC 382
Db 21 PheSerLysArgGlnGlyLeuValGlnLeuValGlnLeuValGlnLeuValGlnLeuVal 40
QY 383 GCGAGAGTCCCGCATGCTCTTCTCCCGCAAGGCAAGCTATGATGATGACCGCAGC 442
Db 41 AlaeGluValAlaValIleValIleValIleValIleValIleValIleValIleValIleVal 60
QY 443 TCCAGCATGACCAAAATTTCTTGAACGTTATGAGCGCTACTTATGCTGAAAAGCTCTT 502
Db 61 SerArgMetAspLysIleLeuGlnArgGlyArgGlyArgGlyArgGlyArgGlyArgGlyArg 80
QY 503 ATTTCAGCTGAATCTGAAAGTGAAGGGAATTTGGTCCGCAAGTACAGAACTTAAGCG 562
Db 81 IleSerIleGlnSerGlnSerGlnSerGlnSerGlnSerGlnSerGlnSerGlnSerGlnSer 100
QY 563 AAGATTGAGACCATACAAAATGTCAACAG 592
Db 101 LysIleGlnThrIleGlnArgCysHisLys 110

RESULT 7

Q947B8 PRELIMINARY; PRT; 267 AA.

ID Q947B8
AC Q947B8
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE MADS-box protein FDRMADS3.
GN Oryza sativa (Rice).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Gao Z., Chen R., Jia H., Sun C.;
Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF345911; AA09473.1; -
DR EMBL: AF345911; AA09473.1; -
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRF-TF; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
SQ SEQUENCE 267 AA; 31266 MW; 1003B3419DED35CD CRC64;

Alignment Scores:
Pred. No.: 2.57e-41 Length: 267
Score: 549.00 Matches: 106
Percent Similarity: 97.27% Conservative: 1
Best Local Similarity: 96.36% Mismatches: 3
Query Match: 53.30% Indels: 0
Gaps: 0

US-10-020-338-8 (1-593) x Q947B8 (1-267)

QY 263 ATGGGTGCGGCAAGGTGACCTGAGCGGATAGAGAACAGATTAATCGCAGGTGACC 322
Db 1 MetGlyArgGlyValGlnLeuValArgIleGlnAsnValIleAsnArgGlnValThr 20
QY 323 TTCTCCAAAGCGCGCAACGGGCTCTGGAAGAGCGGACGAGATCTCGCTCTGTGAC 382
Db 21 PheSerLysArgGlnGlyLeuValGlnLeuValGlnLeuValGlnLeuValGlnLeuVal 40
QY 383 GCGAGAGTCCCGCATGCTCTTCTCCCGCAAGGCAAGCTATGATGATGACCGCAGC 442
Db 41 AlaeGluValAlaValIleValIleValIleValIleValIleValIleValIleValIleVal 60
QY 443 TCCAGCATGACCAAAATTTCTTGAACGTTATGAGCGCTACTTATGCTGAAAAGCTCTT 502
Db 61 SerArgMetAspLysIleLeuGlnArgGlyArgGlyArgGlyArgGlyArgGlyArgGlyArg 80
QY 503 ATTTCAGCTGAATCTGAAAGTGAAGGGAATTTGGTCCGCAAGTACAGAACTTAAGCG 562
Db 81 IleSerIleGlnSerGlnSerGlnSerGlnSerGlnSerGlnSerGlnSerGlnSerGlnSer 100
QY 563 AAGATTGAGACCATACAAAATGTCAACAG 592
Db 101 LysIleGlnThrIleGlnArgCysHisLys 110

DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 KW DNA-binding; Nuclear protein; Transcription regulation.
 SQ SEQUENCE 273 AA; 31248 MW; CA79FIDDC39DC3F0 CRC64;

Alignment Scores:

Pred. No.: 2,116-42 Length: 273
 Score: 561.00 Matches: 109
 Percent Similarity: 99.09% Conservative: 0
 Best Local Similarity: 99.09% Mismatches: 1
 Query Match: 54.47% Indels: 0
 DB: 10 Gaps: 0

US-10-020-338-8 (1-593) x Q41829 (1-273)

QY 263 ATGGGTGGCGGCAAGGTGACGTGAAGCGGATAGAGAAACAGATTAATCGGAGGTGAC 322
 1 MetGlyArgGlyValGlnLeuLysArgIleGlnLeuLysIleAsnArgGlnValThr 20
 DB 323 TTCTCCAGCGCGCGCAAGCGGCTCTGAAGAGCGGCAAGATCTCCGTCTCTGTGAC 382
 21 PheSerLysArgArgAsnGlyLeuLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40
 QY 383 GCGAGGTGCGCGTCATGCTCTTCTCCCGCAAGGCAAGCTCTATAGTACGCCACGAC 442
 41 AlaGluValAlaValIleValIleValPheSerProLysGlyLysLeuLysGlnLysAlaThrAsp 60
 DB 443 TCCAGCATGACAAATTTCTTGAAGCTTATGAGCGCTACTCTTATGCTGAAGAGCTCTT 502
 61 SerArgMetAspLysIleLeuGlnArgGlyGlnArgLysSerValAlaGlnLysAlaLeu 80
 QY 503 ATTGAGTGAATCTGAAGAGTGAAGAAATGCTGCCAGATTAAGGAAATTTAAGCG 562
 81 IleSerAlaGlnSerGlnSerGlnLysAsnTrpCysHisGlnLysLeuLysAla 100
 DB 563 AAGATTGAGACCATCAAAAATGTCACAAG 592
 101 LysIleGlnThrIleGlnLysCysHisLys 110

RESULT 4

ID Q9XJ63 PRELIMINARY; PRT; 267 AA.
 AC Q9XJ63;

DT 01-NOV-1999 (TREMBLrel. 12, Created)
 RC 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 RT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 OS MADS box-like protein.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzae; Oryza.
 NC NCB1_TaxID=4530;

SEQUENCE FROM N.A.

RP STRAIN-CV_NIPONBARE; TISSUE=PANICLE AT PRE-MEIOITIC STAGE;
 RC Shinzuka Y., Yamamoto K., Sasaki T.;
 RT "Characterization of rice MADS box-like genes."
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB003325; BAA81883.1; -
 DR HSSP; P11831; ISRS.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 SQ SEQUENCE 267 AA; 30391 MW; 5A31330C64180D92 CRC64;

Alignment Scores:
 Pred. No.: 4,856-42 Length: 267
 Score: 557.00 Matches: 108
 Percent Similarity: 98.18% Conservative: 0
 Best Local Similarity: 98.18% Mismatches: 2
 Query Match: 54.08% Indels: 0
 DB: 10 Gaps: 0

US-10-020-338-8 (1-593) x Q9XJ63 (1-267)

QY 263 ATGGGTGGCGGCAAGGTGACGTGAAGCGGATAGAGAAACAGATTAATCGGAGGTGAC 322
 1 MetGlyArgGlyValGlnLeuLysArgIleGlnLeuLysIleAsnArgGlnValThr 20
 DB 323 TTCTCCAGCGCGCGCAAGCGGCTCTGAAGAGCGGCAAGATCTCCGTCTCTGTGAC 382
 21 PheSerLysArgArgAsnGlyLeuLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40
 QY 383 GCGAGGTGCGCGTCATGCTCTTCTCCCGCAAGGCAAGCTCTATAGTACGCCACGAC 442
 41 AlaGluValAlaValIleValIleValPheSerProLysGlyLysLeuLysGlnLysAlaThrAsp 60
 DB 443 TCCAGCATGACAAATTTCTTGAAGCTTATGAGCGCTACTCTTATGCTGAAGAGCTCTT 502
 61 SerArgMetAspLysIleLeuGlnArgGlyGlnArgLysSerValAlaGlnLysAlaLeu 80
 QY 503 ATTGAGTGAATCTGAAGAGTGAAGAAATGCTGCCAGATTAAGGAAATTTAAGCG 562
 81 IleSerAlaGlnSerGlnSerGlnLysAsnTrpCysHisGlnLysLeuLysAla 100
 DB 563 AAGATTGAGACCATCAAAAATGTCACAAG 592
 101 LysIleGlnThrIleGlnLysCysHisLys 110

RESULT 5

ID Q9SEW9 PRELIMINARY; PRT; 267 AA.
 AC Q9SEW9;

DT 01-MAY-2000 (TREMBLrel. 13, Created)
 RC 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 RT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 OS MADS15 protein.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzae; Oryza.
 NC NCB1_TaxID=4530;

SEQUENCE FROM N.A.

RP TISSUE=FLOWER;
 RC MEDLINE=99373407; PubMed=10444103;
 RA Moon Y.H., Kang H.G., Jung J.Y., Jeon J.S., Sung S.K., An G.;
 RT "Determination of the motif responsible for interaction between the
 rice APERIAL/AAIMOUS-LIKE9 family proteins using a Yeast two-hybrid
 system."
 RL Plant Physiol. 120:1193-1204(1999).
 DR EMBL; AF058698; AAF19048.1; -
 DR HSSP; P11831; ISRS.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 SQ SEQUENCE 267 AA; 30415 MW; 80B1770C60584ABF CRC64;

Alignment Scores:

Pred. No.: 4,856-42 Length: 267
 Score: 557.00 Matches: 108
 Percent Similarity: 98.18% Conservative: 0
 Best Local Similarity: 98.18% Mismatches: 2
 Query Match: 54.08% Indels: 0

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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 24, 2003, 14:06:48 ; Search time 48 Seconds

(without alignments)
5091.081 Million cell updates/sec

Title: US-10-020-338-8

Perfect score: 1030
Sequence: 1 cccggtcgaccagcagtcgcg.....catcaaaaatgctacaagc 593

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

arched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2.1/USPRO.spool/US10020338/funat.24062003.102354.21507/app.query.fasta_1.775
-DB=SPTRMBL.21 -GFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pico -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USPR=US10020338 @CGN 1.1.138 @funat.24062003.102354.21507 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESUBSTRY -NEG_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -RGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPTRMBL.21: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	566	55.0	276	10	Q9LEI0	Q9LEI0 hordeum vul

2	565	54.9	261	10	Q9ZT76	Q9ZT76 lolium tenu
3	561	54.5	273	10	Q41829	Q41829 zea mays (m
4	557	54.1	267	10	Q9XJ63	Q9XJ63 oryza sativ
5	557	54.1	267	10	Q9SEW9	Q9SEW9 oryza sativ
6	554	53.8	270	10	Q9FRR4	Q9FRR4 zea mays (m
7	549	53.3	267	10	Q947B8	Q947B8 oryza sativ
8	539	52.3	228	10	Q04068	Q04068 sorghum bic
9	515	50.0	246	10	Q9MAY7	Q9MAY7 oryza sativ
10	507	49.2	245	10	Q9ZT77	Q9ZT77 lolium tenu
11	507	49.2	246	10	Q9SEX0	Q9SEX0 oryza sativ
12	505	49.0	246	10	Q9MTC6	Q9MTC6 oryza sativ
13	503	48.8	244	10	Q82128	Q82128 eritricum ae
14	484	47.0	244	10	Q9LEI2	Q9LEI2 hordeum vul
15	446	43.3	243	10	Q93939	Q93939 betula verr
16	445	43.2	240	10	Q948U1	Q948U1 magnolia pr
17	441	42.8	240	10	Q9AR13	Q9AR13 pismum sativ
18	440	42.7	247	10	Q9SXX1	Q9SXX1 dendrobium
19	437	42.4	239	10	Q82695	Q82695 malus domes
20	433	42.0	248	10	Q38742	Q38742 antiirrhinum
21	428	41.6	254	10	Q9XEL0	Q9XEL0 sinapis alb
22	428	41.6	256	10	Q96356	Q96356 brassica ol
23	424	41.2	251	10	Q9SEG1	Q9SEG1 arabidopsis
24	421	40.9	242	10	Q9XHR8	Q9XHR8 nicotiana t
25	421	40.9	252	10	Q941M9	Q941M9 antiirrhinum
26	420	40.8	246	10	Q9SBQ1	Q9SBQ1 petunia hyb
27	420	40.8	256	10	Q96355	Q96355 brassica ol
28	418	40.6	244	10	Q93401	Q93401 betula verr
29	418	40.6	260	10	Q93400	Q93400 betula verr
30	416	40.4	242	10	Q9ZTV2	Q9ZTV2 nicotiana t
31	415	40.3	256	10	Q39371	Q39371 brassica ol
32	415	40.3	257	10	Q41356	Q41356 silene laci
33	413	40.1	205	10	Q9FUI2	Q9FUI2 eucalyptus
34	413	40.1	245	10	Q9FUI2	Q9FUI2 eucalyptus
35	412	40.0	255	10	Q9ZRA5	Q9ZRA5 malus domes
36	410	39.8	244	10	Q9FUI3	Q9FUI3 eucalyptus
37	409	39.7	244	10	Q86415	Q86415 lycopersico
38	409	39.7	245	10	Q9ZTV3	Q9ZTV3 nicotiana t
39	408	39.6	245	10	Q9XHR7	Q9XHR7 capsicum an
40	407	39.5	247	10	Q9SEG7	Q9SEG7 capsicum an
41	402.5	39.1	245	10	Q9SBO0	Q9SBO0 petunia hyb
42	402	39.0	246	10	Q41355	Q41355 silene laci
43	401.5	39.0	248	10	Q8RYR0	Q8RYR0 helianthus
44	400	38.8	242	10	Q9XHR6	Q9XHR6 nicotiana s
45	400	38.8	245	10	Q9A7E2	Q9A7E2 petunia hyb

ALIGNMENTS

RESULT 1

ID	Q9LEI0	PRELIMINARY;	PRT;	276 AA.
AC	Q9LEI0			
DT	01-OCT-2000 (TREMURel. 15, Created)			
DT	01-OCT-2000 (TREMURel. 15, Last sequence update)			
DT	01-JUN-2002 (TREMURel. 21, Last annotation update)			
DE	MADS-box protein 8.			
GN	M8.			
OS	Hordeum vulgare (Barley).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;			
OC	Triticeae; Hordeum.			
OX	NCBI_Taxid=4513;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CV. ATLAS; TISSUE=FLOWER;			
RX	MEDLINE=20346590; PubMed=10890536;			
RA	Schultz J., Franzen R., Nguyen T., Garcia-Maroto F., Pozzi C.,			
RA	Salamini F., Rohde W.;			
RT	"Cloning, mapping and expression analysis of six barley MADS-box			
RT	genes";			
RL	Plant Mol. Biol. 42:899-913(2000).			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
CC	-1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.			

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Qy 263 ATGGGTCGGCAGGTGCACTGAGCCGATAGAGAA CAAGATAAATCGGCAGGTGACC 322

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Db 1 MetGlyArGlyArValaGluLeuLysArgIleGluLysLeuLysIleAsnArgGlnValThr 20
Qy 323 TTCTCCAGCGCGCGCAACGGGCTCTGAAAGAGCGACAGATCTCCGCTCTGTGAC 382
Db 21 PheAlaLysArgArgAsnGlyLeuLeuLysLysAlaTyrGluLeuSerValLeuLysAsp 40
Qy 383 GCGAGGTGCGCGCATGCTCTTCTCCCAAGGCAAGCTTATAGTACGCCAGC 442
Db 41 AlagIValaSerLeuIleValaPheSerAsnArgGlyLysLeuTyrGluPheCysSerThr 60
Qy 443 TCCAGCATGACAAATTTCTTAAGCTATGAGCCCTACTCTTATGCTGAAAAGCTCTT 502
Db 61 SerAsnMetLeuLysThrLeuGlnArgTyrGlnLysCysSerTyrGlySerIleGluVal 80
Qy 503 ATTTCAGTCGATCTGAAGTGAAGTGAAGTATGTCGCCAGATACAGAAAATTAAAGCG 562
Db 81 AsnAsnLysProAlaLysGluLeuGlnLysAsnSerTyrArgGluTyrLeuLysLeuLysGly 100
Qy 563 AAGATTGAGACCATACAAA 583
Db 101 ArgTyrGluAsnLeuGlnArg 107

RESULT 12
AGL9_LYCES
ID AGL9_LYCES STANDARD; PRT; 224 AA.
AC 042464;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL9 homolog (TMS).
GN TMS.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasteride I; Solanales; Solanaceae; Solanum.
CX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. VENT Cherry; TISSUE=flower;
RX MEDLINE=93251098; PubMed=1688249;
RA Punell L., Abu-Abeid M., Zamir D., Nacken W., Schwarz-Sommer Z.,
RA Lifschitz E.;
RT "The MADS box gene family in tomato: temporal expression during
RT floral development, conserved secondary structures and homology with
RT homeotic genes from Antirrhinum and Arabidopsis.";
RL Plant J. 1:255-266(1991).
CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR ACTIVE IN INFLORESCENCE
CC DEVELOPMENT AND FLORAL ORGANOGENESIS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- TISSUE SPECIFICITY: FLOWER-SPECIFIC.
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X60758; CAA43170.1; -
DR EMBL; X60480; CAA43010.1; -
DR HSSP; P11746; INMN.
DR TRANSFAC; T03187; -
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF00319; SRF-TF; 1.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.

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DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KM Transcription regulation; DNA-binding; Nuclear.protein.
FT DOMAIN 3 57 MADS.
FT DOMAIN 98 170 K-BOX.
SQ SEQUENCE 224 AA; 25999 MW; 51D10D30867D06F7 CRC64;

Alignment Scores:
Pred. No.: 1,04e-17 Length: 224
Score: 319.50 Matches: 66
Percent Similarity: 76.58% Conservative: 19
Best Local Similarity: 59.46% Mismatches: 25
Query Match: 31.02% Indels: 1
DB: 1 Gaps: 1

US-10-020-338-8 (1-593) x AGL9_LYCES (1-224)
Qy 263 ATGGGTGCGCGCAAGGTGACGCTGAAGCGATAGAGAACAAATGCGACGTGAC 322
Db 1 MetGlyArGlyArValaGluLeuLysArgIleGluLysLeuLysIleAsnArgGlnValThr 20
Qy 323 TTCTCCAGCGCGCGCAACGGGCTCTGAAAGAGCGACAGATCTCCGCTCTGTGAC 382
Db 21 PheAlaLysArgArgAsnGlyLeuLeuLysLysAlaTyrGluLeuSerValLeuLysAsp 40
Qy 383 GCGAGGTGCGCGCATGCTCTTCTCCCAAGGCAAGCTTATAGTACGCCAGC 442
Db 41 AlagIValaSerLeuIleValaPheSerAsnArgGlyLysLeuTyrGluPheCysSerThr 60
Qy 443 TCCAGCATGACAAATTTCTTAAGCTATGAGCCCTACTCTTAT---GCTGAAAAGCT 499
Db 61 SerSerMetLeuLysThrLeuGlnArgTyrGlnLysCysAsnTyrGlyAlaProGluPro 80
Qy 500 CTTATTCAGTCGATCTGAAGTGAAGTGAAGTATGTCGCCAGATACAGAAAATTAAAG 559
Db 81 AsnLysSerThrArgGluAlaLeuGlnLysSerSerGlnGlnGlnTyrLeuLysLeuLys 100
Qy 560 GCGAAGATTGAGACCATACAAAATGTACAA 592
Db 101 GlyArgTyrGluAlaLeuGlnArgSerGlnArg 111

RESULT 13
AGL9_SINAP
ID AGL9_SINAP STANDARD; PRT; 254 AA.
AC 004067;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL9 homolog (MADS D).
GN AGL9.
OS Sinapis alba (White mustard) (Brassica hirta).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Sinapis.
CX NCBI_TaxID=3728;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=flower;
RX MEDLINE=97390682; PubMed=9247539;
RA Bonhomme F., Sommer H., Bernier G., Jacquard A.;
RT "Characterization of SAMDS D from Sinapis alba suggests a dual
RT function of the gene: in inflorescence development and floral
RT organogenesis.";
RL Plant Mol. Biol. 34:573-573(1997).
CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR ACTIVE IN INFLORESCENCE
CC DEVELOPMENT AND FLORAL ORGANOGENESIS.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC -----
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QY 383 GCGAGGTGCGCTATCTTCTCCCAAGCAAGCTATAGTACGCCACGAC 442
 Db 41 AlagluValAlaleuilellepheserAarglyLysleuTyrgluPheCysSerThr 60
 QY 443 TCCAGCATGACCAAAATTTGTAAGCTTATGCTTATGCTGAAAGGCTCTT 502
 Db 61 SerCysMetAsnLysThrleuGlnArgCysSerTyrglySerleuGlnThr 80
 QY 503 ATTTCAGCTGAATCGAAGGAAATGTCGCCAAGTACAGAACTTAAGGCG 562
 Db 81 SerGlnProSerTyrglyThrGlnSerSerTyrglyGlnTyrlleuLysleuYsala 99
 QY 563 AAGATTGAGACCATACAAAATGTCACAG 592
 Db 100 LysValAspValleuGlnArgSerHisArg 109

RESULT 9
 AGL9_PETHY
 ID AGL9_PETHY STANDARD; PRT; 241 AA.
 QY 003489;
 01-FEB-1995 (Rel. 31, Created)
 01-FEB-1996 (Rel. 33, Last sequence update)
 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Agamous-like MADS box protein AGL9 homolog (Floral homeotic protein FBP2) (Floral binding protein 2).
 GN FBP2.
 OS Petunia hybrida (Petunia).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
 ON NCBI_TaxID=4102;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93005737; PubMed=1356537;
 RA Angenent G.C., Buscher M., Franken J., Mol J.N.M., van Tunen A.J.;
 RT "Differential expression of two MADS box genes in wild-type and mutant petunia flowers.";
 RL Plant Cell 4:983-993(1992).
 RN [2]
 RP REVISIONS TO C-TERMINUS.
 RA Angenent G.C.;
 RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
 CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.

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 CC
 CC EMBL; M91666; AAA86854.1; -
 DR PIR; J01690; J01690.
 DR HSSP; P11746; 1MMN.
 DR TRANSFAC; T03093; -
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF00319; SRF-TF; 1.
 DR Pfam; PF01486; K-box; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 KW Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 3 57 MADS
 FT 98 170 K-BOX.
 SO SEQUENCE 241 AA; 27562 MW; B575BE946BD310BB CRC64;

Alignment Scores:
 Pred. No.: 1,43e-18 Length: 241
 Score: 330.50 Matches: 68
 Percent Similarity: 78.38% Conservative: 19
 Best Local Similarity: 61.26% Mismatches: 23
 Query Match: 32.09% Indels: 1
 Gaps: 1

US-10-020-338-8 (1-593) x AGL9_PETHY (1-241)
 QY 263 ATGGGTGCGGCGGACGTGACGCGATAGAGCAAGATTAATCGGAGTGAC 322
 Db 1 MetGlyArgGlyArgValGlnLeuLysArgGlyLeuLysLysIleAsnArgGlnValThr 20
 QY 323 TTCTCAAGCGCGCCCAACGGGCTCTGTAAGAGCGACGAGATCTCGTCTGTGAC 382
 Db 21 PheAlaLysArgAlaGlnGlyLeuLeuLysLysAlaTyrgluLeuSerValLeuCyasp 40
 QY 383 GCGAGGTGCGGCTATCTTCTCCCAAGCAAGCTTATAGTACGCCACGAC 442
 Db 41 AlagluValAlaleuilellepheserAarglyLysleuTyrgluPheCysSerThr 60
 QY 443 TCCAGCATGACCAAAATTTGTAAGCTTATGCTTATGCTGAAAGGCTCTT 499
 Db 61 SerSerMetLeuLysThrleuGlnArgTyrglnLysCysSerTyrglyAlaProGluThr 80
 QY 500 CTATTTTCAGCTGAATCGAAGGAAATGTCGCCAAGTACAGAACTTAAG 559
 Db 81 AsnIleSerThrArgGluAlaLeuGlnIleSerSerGlnGlnTyrlleuLysleuLys 100
 QY 560 GCGAAGATTGAGACCATACAAAATGTCACAG 592
 Db 101 AlaArgTyrgluAlaLeuGlnArgSerGlnArg 111

RESULT 10
 AGL2_ARATH
 ID AGL2_ARATH STANDARD; PRT; 248 AA.
 AC P29382;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Agamous-like MADS box protein AGL2.
 GN AGL2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 ON NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91160981; PubMed=1672119;
 RA Ma H., Yanofsky M.F., Meyerowitz E.M.;
 RT "AGL1-AGL6, an Arabidopsis gene family with similarity to floral homeotic and transcription factor genes.";
 RL Genes Dev. 5:484-495(1991).
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED EARLY DURING FLOWER DEVELOPMENT.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
 CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.

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 CC
 CC EMBL; M55551; AAA32732.1; -
 DR PIR; B39534; B39534.
 DR HSSP; P11746; 1MMN.

RP FUNCTION, AND TISSUE SPECIFICITY.
 RC STRAIN=cv. Landsberg erecta;
 RX MEDLINE=98171466; PubMed=9502732;
 RA Gu Q., Ferrandiz C., Yanofsky M.F., Marcijnsen R.;
 RT "The FRUITFULL MADS-box gene mediates cell differentiation during
 Arabidopsis fruit development."; Development 125:1509-1517(1998).
 RL Development 125:1509-1517(1998).
 CC -1- FUNCTION: Probable transcription factor required for normal
 pattern of cell division, expansion and differentiation during
 morphogenesis of the silique.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- TISSUE SPECIFICITY: Vascular tissue of cauline leaves, floral
 shoot apex and valves of carpels and fruits.
 CC -1- INDUCTION: Dramatically up-regulated upon the transition from
 vegetative to reproductive development.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 FACTORS.
 CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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 CC -----
 DR EMBL; U33473; AAA97403.1; -;
 DR EMBL; AB008269; BAB10640.1; -;
 DR EMBL; AF386929; AAK62374.1; -;
 DR EMBL; AY072463; AAL66878.1; -;
 DR HSSP; P11746; 1MMN.
 DR TRANSFAC; T03030; -;
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF00319; SRF-TF; 1.
 DR Pfam; PF01486; K-box; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 DR Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 3 57 MADS.
 FT DOMAIN 97 169 K-BOX.
 SQ SEQUENCE 242 AA; 27536 MW; 516499731EADB2D2 CRC64;
 Alignment Scores:
 Pred. No.: 6.2e-24 Length: 242
 Score: 399.00 Matches: 75
 Percent Similarity: 85.98% Conservative: 17
 Best Local Similarity: 70.09% Mismatches: 15
 Query Match: 38.74% Indels: 0
 DB: 1 Gaps: 0
 US-10-020-338-8 (1-593) x AGL8_ARATH (1-242)
 QY 263 ATGGTCCGCGGACAGTGCAGTGAAGCGGATAGAGAAACATATAATTCGGAGTGACC 322
 Db 1 MetGlyArgGlyArgValGlnLeuLysArgIleGlnAsnLysIleAsnArgGlnValThr 20
 QY 323 TTCTCAAGCGCGGACGAGGCTCTGAAGAAGCGACGAGATCCGCTCTGTGAC 382
 Db 21 PheSerLysArgArgSerGlyLeuLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40
 QY 383 GCGAGGTGCGCGTATGCTCTTCTCCCAAGGCAAGCTATGATGAGCCACGAC 442
 Db 41 AlaGlnValAlaLeuIleValPheSerSerLysGlyLysLeuPheGlnLysSerThrAsp 60
 QY 443 TCCACAGCGACAAATCTTGAACGTATGAGCGCTACTTAACTGCAAAAGCTCTT 502
 Db 61 SerCysMeGlnArgIleLeuGlnArgIleLysArgPargIleLysLysSerValGlnLeu 80
 QY 503 ATTGAGCTGATCGAAAGTGAAGGAAATTTGTCGCCAGATACAGAACTTAAGCG 562

Db 81 ValGlyArgAspValSerGlnSerGlnAsnTriPValLeuGlnHISAlaLysLeuLysAla 100
 QY 563 AAGATTGAGACCATACAAAA 583
 Db 101 ArgValGlnValLeuGlnLys 107
 RESULT 8
 CMBL DIACA
 ID CMBL DIACA STANDARD; PRT; 233 AA.
 AC Q3685;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE MADS box protein CMBL.
 GN CMBL.
 OS Dianthus caryophyllus (Carnation) (Clove pink).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Dianthus.
 CX NCBI_TaxID=3570;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Scania; TISSUE=Petal;
 RA Baudinette S.C., Savin K.W.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 FACTORS.
 CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
 CC -----
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 CC -----
 DR EMBL; L40404; AAA62761.1; -;
 DR HSSP; P11746; 1MMN.
 DR TRANSFAC; T03060; -;
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF00319; SRF-TF; 1.
 DR Pfam; PF01486; K-box; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 DR Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 3 58 MADS.
 FT DOMAIN 96 168 K-BOX.
 SQ SEQUENCE 233 AA; 26888 MW; CB8765618466151A CRC64;
 Alignment Scores:
 Pred. No.: 2.26e-20 Length: 233
 Score: 353.50 Matches: 69
 Percent Similarity: 80.00% Conservative: 19
 Best Local Similarity: 62.73% Mismatches: 21
 Query Match: 34.32% Indels: 1
 DB: 1 Gaps: 1
 US-10-020-338-8 (1-593) x CMBL DIACA (1-233)
 QY 263 ATGGTCCGCGGACAGTGCAGTGAAGCGGATAGAGAAACATATAATTCGGAGTGACC 322
 Db 1 MetGlyArgGlyArgValGlnLeuLysArgIleGlnAsnLysIleAsnArgGlnValThr 20
 QY 323 TTCTCAAGCGCGGACGAGGCTCTTGAAGAAGCGACGAGATCCGCTCTGTGAC 382
 Db 21 PheAlaLysArgArgGlnGlyLeuLeuLysLysAlaLysArgIleLysSerValLeuLysAsp 40

NCBI_TaxID=4081;
[1]
SEQUENCE FROM N.A.
STRAIN=cv. VENT Cherry; TISSUE=Flower;
MEDLINE=93251098; PubMed=1688249;
RA Pnueli L., Abu-Abeid M., Zamir D., Nacken W., Schwarz-Sommer Z.,
Lifschitz E.;
RT "The MADS box gene family in tomato: temporal expression during
RT floral development, conserved secondary structures and homology with
RT homeotic genes from Antirrhinum and Arabidopsis.";
RL Plant J. 1:255-266(1991).
CC - FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC - SUBCELLULAR LOCATION: Nuclear (By similarity).
CC - TISSUE SPECIFICITY: FLOWER-SPECIFIC.
CC - SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC - SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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CC
CC EMBL; X60757; CAA43169.1; -
CC HSSP; P11746; 1NMN.
CC TRANSFAC; T03186; -
CC InterPro; IPR002487; TF_Kbox.
CC InterPro; IPR002100; TF_MADSbox.
CC Pfam; PF00319; SRF-TF; 1.
CC Pfam; PF01486; K-box; 1.
CC PRINTS; PR00404; MADSDOMAIN.
CC SMART; SM00432; MADS; 1.
CC PROSITE; PS00350; MADS_BOX_1; 1.
CC PROSITE; PS00066; MADS_BOX_2; 1.
CC KW Transcription regulation; DNA-binding; Nuclear protein.
CC FT DOMAIN 3 57 MADS.
CC FT 97 169 K-BOX.
CC SQ SEQUENCE 227 AA; 26403 MW; 4976195B3BDE53F5 CRC64;

Alignment Scores:
Pred. No.: 1,22e-24 Length: 227
Score: 408.00 Matches: 79
Percent Similarity: 85.45% Conservative: 15
Best Local Similarity: 71.82% Mismatches: 16
Indels: 0
Gaps: 0
Query Match: 1 39.61%
US-10-020-338-8 (1-593) x AG18_LYC8S (1-227)
OY ATGGGTGCGGCGAGCTGAGCGATGAGAAAGATTAATCGGAGGTGACC 322
DB 1 MetGlyArgGlyArgValGlnLeuLysArgIleGlnLysValLeuAsnArgGlnValThr 20
OY 323 TTCTCAAGCCCGCGAAGCGGCTCTGAAAGAGCGGACGAGATCTCGTCTCTGTGAC 382
DB 21 PheSerLysArgArgSerGlyLeuLeuLysLysAlaHisGlnIleSerValLeuGlyAsp 40
OY 383 GCGGAGGTGCGGCGATGCTCTTCCCGCAAGGACGCTTATGAGAGCGGACGAC 442
DB 41 AlaGlnValGlyLeuIleValPheSerThrLysGlyLysLeuPheGlnLysAlaAsnAsp 60
OY 443 TTCACATGAGCAAAATTTCTGAACGTATGAGCGCTACTTATGCTGAAAAGCTCTT 502
DB 61 SerGlyMetGluArgIleLeuGlnLysArgTyrGlnLysArgTyrSerPheAlaGlnLysGlnLeu 80
OY 503 ATTGAGCTGATCTGAAGAGTGAAGGAATTTGTCACGATTAAGGAAATTTAAGCG 562
DB 81 ValProThrAspHisThrSerProValSerThrPThrLeuGlnLysAlaArgLysLeuLysAla 100
OY 563 AAGATTGAGACCATCAAAATATGTCAAG 592

DB 101 ArgLeuGlnValLeuGlnArgGlnGlnLys 110
RESULT 5
AG18_SOLUTU STANDARD; PRT; 250 AA.
AC 042429;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Agamous-like MADS box protein AG18 homolog (POTM1-1).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
CC NCBI_TaxID=4113;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=cv. Superior;
CC MEDLINE=96343939; PubMed=8756601;
CC Kang S.G., Hannapel D.J.;
CC "A novel MADS-box gene of potato (Solanum tuberosum L.) expressed
CC during the early stages of tuberization.";
CC Plant Mol. Biol. 31:379-386(1996).
CC RL - FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC - SUBCELLULAR LOCATION: Nuclear (By similarity).
CC - SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC - SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U23758; AAA92840.1; -
CC EMBL; U23757; AAA92839.1; -
CC HSSP; P11746; 1NMN.
CC TRANSFAC; T03145; -
CC InterPro; IPR002487; TF_Kbox.
CC InterPro; IPR002100; TF_MADSbox.
CC Pfam; PF00319; SRF-TF; 1.
CC Pfam; PF01486; K-box; 1.
CC PRINTS; PR00404; MADSDOMAIN.
CC SMART; SM00432; MADS; 1.
CC PROSITE; PS00350; MADS_BOX_1; 1.
CC PROSITE; PS00066; MADS_BOX_2; 1.
CC KW Transcription regulation; DNA-binding; Nuclear protein.
CC FT DOMAIN 3 57 MADS.
CC FT 97 169 K-BOX.
CC SQ SEQUENCE 250 AA; 28922 MW; EDE37FFFE793DDC4 CRC64;

Alignment Scores:
Pred. No.: 1.76e-24 Length: 250
Score: 406.00 Matches: 77
Percent Similarity: 85.45% Conservative: 17
Best Local Similarity: 70.00% Mismatches: 16
Indels: 0
Query Match: 1 39.42%
Gaps: 0
US-10-020-338-8 (1-593) x AG18_SOLUTU (1-250)
OY 263 ATGGGTGCGGCGAGCTGAGCGATGAGAAAGATTAATCGGAGGTGACC 322
DB 1 MetGlyArgGlyArgValGlnLeuLysArgIleGlnLysValLeuAsnArgGlnValThr 20
OY 323 TTCTCAAGCCCGCGAAGCGGCTCTGAAAGAGCGGACGAGATCTCGTCTCTGTGAC 382
DB 21 PheSerLysArgArgSerGlyLeuLeuLysLysAlaHisGlnIleSerValLeuGlyAsp 40

DR PROSITE; PS50066; MADS_BOX_2; 1.
 KW Transcription regulation; DNA-binding; Activator; Nuclear protein;
 KM Developmental protein; Polymorphism.
 FT DOMAIN 3
 FT 97 169 MADS.
 FT 57 K-BOX.
 FT 85 S -> P (IN STRAIN CV. CHI-1).
 FT 93 M -> T (IN STRAIN CV. BLA-1).
 FT 99 M -> R (IN STRAIN CV. CHI-1).
 FT 100 A -> T (IN STRAIN CV. LER).
 FT 120 M -> V (IN STRAIN CV. JL-1).
 FT 125 L -> P (IN STRAIN CV. BLA-1).
 FT 126 S -> G (IN STRAIN CV. JL-1).
 FT 166 L -> P (IN STRAIN CV. CHI-1).
 FT 212 L -> P (IN STRAIN CV. CHI-1).
 FT 233 A -> V (IN STRAIN CV. CO-1).
 FT 184 E -> G (IN REF. 3; AM28458).
 FT 236 MISSING (IN REF. 1).
 SQ CONFLICT 236
 SEQUENCE 256 AA; 30182 MW; 01E26D18CE3478C CRC64;

Alignment Scores:

Pred. No.: 6,85e-26 Length: 256
 Score: 424.00 Matches: 82
 Percent Similarity: 88.79% Conservative: 13
 Best Local Similarity: 76.64% Mismatches: 12
 Query Match: 41.17% Indels: 0
 DB: 1 Gaps: 0

US-10-020-338-8 (1-593) x AP1_ARATH (1-256)

OY 263 ATGGGTCGGCGGCAAGTGCGAGTGAAGCGGATGAAGCAAGATAATCGGAGGTGAC 322
 Db 1 MetGlyArgGlyArgValGlnLeuLysArgGlnLeuLysValLeuLysArgGlnValThr 20
 OY 333 TTCTCCAAAGCGCGGCAAGCGGCTCTGGAAGAGGCGCAGAGTCTCCGCTCTGTGAC 382
 Db 21 PheSerLysArgArgAlaGlyLeuLeuLysLysAlaHisGlnLysSerValLeuLysAsp 40
 OY 333 GCGGAGGTGCGGCTATCTCTTCTCCCAAGGCAAGCTTATGAGTACGCCACGAC 442
 Db 41 AlaGlnValAlaLeuValValPheSerHisLysGlyLysLeuPheGlnLysSerThrAsp 60
 OY 443 TCCACATGAGCAAAATTTGTAAGCTATGAGCGCTCTTATGCTGAAGAGCTCTT 502
 Db 61 SerCysMetGlnLysLeuLysGlnArgTyrGlnArgTyrSerTyrAlaGlnArgLysLeu 80
 OY 503 ATTGAGCTGATGTAAGTAAGTGAAGGAATGTCGCCAGATTAAGAACTTAAGGCG 562
 Db 81 IleAlaProGlnSerAspValAsnThrAsnThrPseMetGlnTyrAsnArgLeuLysAla 100
 OY 563 AAGATTGAGACCATACAAA 583
 Db 101 LysIleGlnLeuLeuGlnArg 107

RESULT 3

AGL8_SOLCO STANDARD; PRT; 250 AA.
 ID AGL8_SOLCO
 AC 022328;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Agamous-like MADS box protein AGL8 homolog.
 GN SCM1.
 OS Solanum commersonii (Commerson's wild potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanales; Solanaceae; Solanum.
 OK NCBI_taxonomy4109;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Seppanen M.M.;
 RL Submitted (May-1997) to the EMBL/GenBank/DBD databases.
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION

FACTORS.

-1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.

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 CC or send an email to license@isb-sib.ch).

DR EMBL; AF002666; AAB55161.1; -
 DR HSBP; P11746; IMNM.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF00319; SRF-TF; 1.
 DR Pfam; PF01486; K-box; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 KW Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 3
 FT 97 169 MADS.
 FT 57 K-BOX.
 SQ SEQUENCE 250 AA; 28741 MW; C9871403C23ED5D5 CRC64;

Alignment Scores:

Pred. No.: 8,55e-25 Length: 250
 Score: 410.00 Matches: 79
 Percent Similarity: 85.45% Conservative: 15
 Best Local Similarity: 71.82% Mismatches: 16
 Query Match: 39.81% Indels: 0
 DB: 1 Gaps: 0

US-10-020-338-8 (1-593) x AGL8_SOLCO (1-250)

OY 263 ATGGGTCGGCGGCAAGTGCGAGTGAAGCGGATGAAGCAAGATAATCGGAGGTGAC 322
 Db 1 MetGlyArgGlyArgValGlnLeuLysArgGlnLeuLysValLeuLysArgGlnValThr 20
 OY 333 TTCTCCAAAGCGCGGCAAGCGGCTCTGGAAGAGGCGCAGAGTCTCCGCTCTGTGAC 382
 Db 21 PheSerLysArgArgAlaGlyLeuLeuLysLysAlaHisGlnLysSerValLeuLysAsp 40
 OY 333 GCGGAGGTGCGGCTATCTCTTCTCCCAAGGCAAGCTTATGAGTACGCCACGAC 442
 Db 41 AlaGlnValAlaLeuValValPheSerHisLysGlyLysLeuPheGlnLysSerThrAsp 60
 OY 443 TCCACATGAGCAAAATTTGTAAGCTATGAGCGCTCTTATGCTGAAGAGCTCTT 502
 Db 61 SerCysMetGlnLysLeuLysGlnArgTyrGlnArgTyrSerTyrAlaGlnArgLysLeu 80
 OY 503 ATTGAGCTGATGTAAGTAAGTGAAGGAATGTCGCCAGATTAAGAACTTAAGGCG 562
 Db 81 ValProThrAspHisThrSerProGlnSerThrPheGlnLeuAlaLysLeuLysAla 100
 OY 563 AAGATTGAGACCATACAAAATGTCACAG 592
 Db 101 ArgLeuGlnValLeuGlnArgGlnArgGlnLys 110

RESULT 4

AGL8_LYCES STANDARD; PRT; 227 AA.
 ID AGL8_LYCES
 AC 040170;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Agamous-like MADS box protein AGL8 homolog (TM4).
 GN TDR4.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanales; Solanaceae; Solanum.

DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF00319; SRF-TF; 1.
DR Pfam: PF01486; K-box; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS00066; MADS_BOX_2; 1.
KM Transcription regulation; DNA-binding; Activator; Nuclear protein;
FT Developmental protein.
FT DOMAIN 3 MADS.
FT DOMAIN 169 K-BOX.
SQ SEQUENCE 254 AA; 29918 MW; 187FEDE51BEF743 CRC64;

Alignment Scores:
Pred. No.: 6.85e-26 Length: 254
Score: 424.00 Matches: 82
Percent Similarity: 88.79% Conservative: 13
Best Local Similarity: 76.64% Mismatches: 12
Query Match: 41.17% Indels: 0
Gaps: 0

US-10-020-338-8 (1-593) x API_SINAI (1-254)

QY 263 ATGGGTCGGCGGAGTGCAGTGAAGCGGATGAGCAAGATTAATCGGAGGTGAC 322
Db 1 Metllyatgalyaagvalglnleuylargylleglunhlylshnarglnvalthr 20
QY 323 TTTCACGACGCGCCGCAAGCGGCTCTGTAAGAGGCGACGATCTCCGTCGTGAC 382
Db 21 Pheserlysaragatgalyaaglyleuylshnarglnleuylshnarglnleuylshn 40
QY 383 GCGGAGTGGCGGCGGCTCTGTCCTCCGCAAGCGGATCTGATGATGACCGAC 442
Db 41 Alagluvalalaleuvalvalpheserhlyshnarglnleuylshnarglnleuylshn 60
QY 443 TCCAGCATGAGCAAAATCTTGAACGTATGAGCGCTCTGATGATGAGCGCTCTT 502
Db 61 Serlyshnarglnleuylshnarglnleuylshnarglnleuylshnarglnleuylshn 80
QY 503 ATTTCAGTGAATCTGAAAGTGAAGGAAATGTCGCAAGATCAGGAACTTAAGCGG 562
Db 81 lilelaphroglnsarvalshnthrshnarglnleuylshnarglnleuylshn 100
QY 563 AAGATTGAGACCATACAAA 583
Db 101 Lysileglnleuylshnarglnleuylshnarglnleuylshnarglnleuylshn 107

API_ARATH STANDARD; PRT; 256 AA.
AC P35631; Q9LOA8;
DT 01-JUN-1994 (Rel. 29, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Floral homeotic protein APETALA1 (AGL7 protein).
GN API OR AGL7 OR A1G69120 OR FAN2.9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eudicots II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta;
RX MEDLINE=93063372; PubMed=1359429;
RA Mandel M.A., Gustafson-Brown C., Savidge B., Yanofsky M.F.;
RT "Molecular characterization of the Arabidopsis floral homeotic gene
APETALA1";
RL Nature 360:273-277 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX

RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Felblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hutzar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luos J.S., Maiti R., Marziani A.,
RA Miltischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shin P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utebäck T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana";
RL Nature 408:816-820 (2000).
RN [3]
RP SEQUENCE OF 1-251 FROM N.A.
RC STRAIN=Various strains;
RX MEDLINE=21969421; PubMed=11973317;
RA Olsen K.M., Womack A., Garrett A.R., Suddith J.I., Purugganan M.D.;
RT "Contrasting evolutionary forces in the Arabidopsis thaliana floral
developmental pathway";
RL Genetics 160:1641-1650 (2002).
CC -1- FUNCTION: CONTROLS FLORAL MERISTEM IDENTITY. IS ALSO REQUIRED FOR
CC NORMAL DEVELOPMENT OF SEPAL AND PETAL. IS REQUIRED FOR THE
CC TRANSITION OF AN INFLORESCENCE MERISTEM INTO A FLORAL MERISTEM.
CC INTERACTS WITH LEAFY.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN YOUNG FLOWER PRIMORDIA, LATER
CC BECOMES LOCALIZED TO SEPAL AND PETALS.
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC
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CC
CC EMBL; Z16421; CAA78909.1; -
CC EMBL; ACC08262; AAF27070.1; -
CC EMBL; AF466771; AAM28447.1; -
CC EMBL; AF466772; AAM28448.1; -
CC EMBL; AF466773; AAM28449.1; -
CC EMBL; AF466774; AAM28450.1; -
CC EMBL; AF466775; AAM28451.1; -
CC EMBL; AF466776; AAM28452.1; -
CC EMBL; AF466777; AAM28453.1; -
CC EMBL; AF466778; AAM28454.1; -
CC EMBL; AF466779; AAM28455.1; -
CC EMBL; AF466780; AAM28456.1; -
CC EMBL; AF466781; AAM28457.1; -
CC EMBL; AF466782; AAM28458.1; -
CC EMBL; AF466783; AAM28459.1; -
CC EMBL; AF466784; AAM28460.1; -
CC EMBL; AF466785; AAM28461.1; -
CC HSSP; P11746; INNM.
CC TRANSFAC; T01775; -
CC InterPro: IPR002487; TF_Kbox.
CC InterPro: IPR002100; TF_MADSbox.
CC Pfam; PF00319; SRF-TF; 1.
CC Pfam; PF01486; K-box; 1.
CC PRINTS; PR00404; MADSDOMAIN.
CC SMART; SM00432; MADS; 1.
CC PROSITE; PS00350; MADS_BOX_1; 1.

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submitted to the EMBL Data Library, March 1995
A:Description: Carnation MADS box genes.

A:Reference number: Z17094

A:Accession: T10714

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-233 <BAU>

A:Cross-references: EMBL:L40404; NID:G695316; PID:G695317

A:Experimental source: cv. Scania; petals

C:Genetics:

A:Gene: CMB1

C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

C:Keywords: DNA binding; transcription factor; transcription regulation

F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:
Score: 5.59e-24	233	69	19	21	1
Percent Similarity: 35.3.50					
Percent Local Similarity: 62.73%					
Query Match: 34.32%					
Gaps: 2					

US-10-020-338-8 (1-593) x T10714 (1-233)

```

Oy 263 ATGGGTGCGCGCAAGTGTGACGCTGAGCGGATAGAGCAAGATAATCGGAGGTGACC 322
    |||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 1 MetGlyArgGlyArgValGlnLeuLysArgGlnLeuLysArgGlnLeuLysArgGlnValThr 20

Oy 323 TTCTCCAGCGCGCGCAAGCGGCTCTCTGAAGAGCGGACGAGATCCGCTCTGTGAC 382
    |||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 21 PheSerLysArgGlnValGlnLeuLysArgGlnLeuLysArgGlnLeuLysArgGlnValThr 40

Oy 383 GCGGAGTGGCGGCTGATGCTTCTTCCCGCAAGGCAAGCTGTATGATGACCGAC 442
    |||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 41 AlaGlnValAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60

Oy 443 TCCGACATGACCAAAATTTCTGAACGCTTATGAGCGCTACTTATGCTGAAAAGCTCTT 502
    |||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 61 SerSerMetLysArgGlnValGlnLeuLysArgGlnLeuLysArgGlnLeuLysArgGlnValThr 80

Oy 503 ATTTCAGCTGATCTGAAGAGGGAATTGCTGCGACGAATACGAGAACTTAAGCGC 562
    |||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 81 SerGlnProSerLysGlnValGlnLeuLysArgGlnLeuLysArgGlnLeuLysArgGlnValThr 99

Oy 563 AAGATTGACCATTCACAAATATGTCACAG 592
    |||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 100 LysValAlaSerValLeuGlnArgSerHisArg 109
  
```

RESULT 13

551935

Probable MADS-box protein dal1 - Norway spruce

C:Species: Picea abies (Norway spruce)

C:Date: 14-Jul-1995 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000

C:Accession: T14846; S51935

R:Tandere, K.; Albert, V.A.; Sundas, A.; Engstrom, P.

Plant Mol. Biol. 27, 69-78, 1995

A:Title: Conifer homologues to genes that control floral development in angiosperms.

A:Reference number: S51934; MUID:95170009; PMID:7865797

A:Accession: T14846

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-261 <TAN>

A:Cross-references: EMBL:X80902; NID:G695685; PID:G695686

A:Accession: S51935

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 92-156 <TA2>

C:Genetics:

A:Gene: dal1

C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

C:Keywords: DNA binding; transcription regulation

F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:
Score: 7.01e-24	261	70	16	23	1
Percent Similarity: 352.50					
Percent Local Similarity: 78.18%					
Best Local Similarity: 63.64%					
Query Match: 34.22%					
Gaps: 2					

US-10-020-338-8 (1-593) x S51935 (1-261)

```

Oy 263 ATGGGTGCGCGCAAGTGTGACGCTGAGCGGATAGAGCAAGATAATCGGAGGTGACC 322
    |||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 1 MetGlyArgGlyArgValGlnLeuLysArgGlnLeuLysArgGlnLeuLysArgGlnValThr 20

Oy 323 TTCTCCAGCGCGCGCAAGCGGCTCTCTGAAGAGCGGACGAGATCCGCTCTGTGAC 382
    |||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 21 PheSerLysArgGlnValGlnLeuLysArgGlnLeuLysArgGlnLeuLysArgGlnValThr 40

Oy 383 GCGGAGTGGCGGCTGATGCTTCTTCCCGCAAGGCAAGCTGTATGATGACCGAC 442
    |||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 41 AlaGlnValAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 59

Oy 443 TCCGACATGACCAAAATTTCTGAACGCTTATGAGCGCTACTTATGCTGAAAAGCTCTT 502
    |||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 60 SerSerMetLysArgGlnValGlnLeuLysArgGlnLeuLysArgGlnLeuLysArgGlnValThr 79

Oy 503 ATTTCAGCTGATCTGAAGAGGGAATTGCTGCGACGAATACGAGAACTTAAGCGC 562
    |||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 80 ThrGlyValSerAspArgGlnAlaGlnAsnTrpHisGlnGlnValThrLysLeuLysGly 99

Oy 563 AAGATTGACCATTCACAAATATGTCACAG 592
    |||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 100 LysValAlaGlnLeuLeuGlnArgSerGlnArg 109
  
```

RESULT 14

T09603

MADS-box protein 3 - Monterey pine

C:Species: Pinus radiata (Monterey pine)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jan-2000

C:Accession: T09603

R:Mouradov, A.; Loopstra, C.; Southerton, S.; Glassick, T.; Marshal, H.; Teasdale, R.

submitted to the EMBL Data Library, October 1996

A:Reference number: Z16765

A:Accession: T09603

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-261 <MCU>

A:Cross-references: EMBL:U76726; NID:G2160700; PID:G2160701

A:Experimental source: tissue-type immature male and female cones

C:Genetics:

A:Gene: MADS3

C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homo

C:Keywords: DNA binding; transcription regulation

F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:
Score: 7.01e-24	261	70	16	23	1
Percent Similarity: 352.50					
Percent Local Similarity: 78.18%					
Best Local Similarity: 63.64%					
Query Match: 34.22%					
Gaps: 2					

US-10-020-338-8 (1-593) x T09603 (1-261)

```

Oy 263 ATGGGTGCGCGCAAGTGTGACGCTGAGCGGATAGAGCAAGATAATCGGAGGTGACC 322
    |||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 1 MetGlyArgGlyArgValGlnLeuLysArgGlnLeuLysArgGlnLeuLysArgGlnValThr 20

Oy 323 TTCTCCAGCGCGCGCAAGCGGCTCTCTGAAGAGCGGACGAGATCCGCTCTGTGAC 382
    |||.....|.....|.....|.....|.....|.....|.....|.....|.....|
Db 21 PheSerLysArgGlnValGlnLeuLysArgGlnLeuLysArgGlnLeuLysArgGlnValThr 40
  
```

DB: 2 Gaps: 0

US-10-020-338-8 (1-593) x S71208 (1-242)

OY 263 ATGGGTCCGCGCAGAGTGCAGCTGAAGCGGATAGAGAACAAGATAAATCGCAGGTACC 322
|||||
Db 1 MetGLyArGGLyArGVAlGlInLeuLySArGIleGIuAnLylLSAsnArGSLnValThr 20
323 TTCTCCAAAGCGCCGCAACGGGCTCTGAAGAAAGCGCACAGATGTCCTCGTCTGTAC 382
|||||
Db 21 PheSerLySArGARserGIyLeuLeuLySLAsnIleSGLIILeserValLeuLySasp 40
OY 383 GCGAGAGTGCGCGCTATGCTGTTCTCCCCCAAAGCAAGCTTAAGTAGAGCCAC 442
|||||
Db 41 AlaGIuValAlaLeuIleValPheSerLySGLyLSLeuPheGLuTySerThrSsp 60
OY 443 TCACCATGACAAAATTCTTGAACGTTATGAGCGCTACTTATGCTGAAAAGGCTTT 502
|||||
Db 81 ValGIyArGSArPVAlSerGIuSerGIuSenTrPVAlLeuGLuHlAlAltyLeuLySAla 100
OY 563 AAGATTGAGACCATACAAAA 583
|||
Db 101 ArgValGIuValLeuGLuLyS 107

RESULT 10
T14457
MADS box protein homolog CAL - broccoli;
CISpecies: Brassica oleracea var. botrytis (broccoli)
CDate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
CAccession: T14457
R:Kempin, S.A.; Savidge, B.; Yanofsky, M.F.
Science 267, 522-525, 1995
A>Title: Molecular basis of the cauliflower phenotype in Arabidopsis.
AReference number: Z18101; MUID:95125463; PMID:7824951
AAccession: T14457
A>Status: preliminary; translated from GB/EMBL/DDBJ
AMolecule type: mRNA
AResidues: 1-150 <KEM>
ACross-references: EMBL:L36927; NID:g642592; PINN:AAA64791.1; PID:g642593
AExperimental source: curd (inflorescence meristem)
C:Genetics:
A:Gene: CAL
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homo-
C:Keywords: DNA binding; nucleus; transcription regulation

Alignment Scores:

	Tried. No.:	5.9e-27	Length:	150
OY	Score:	386.00	Matches:	75
	Percent Similarity:	87.62%	Conservative:	17
	Best Local Similarity:	71.43%	Mismatches:	11
	Query Match:	37.48%	Indels:	2
DB:		2	Gaps:	1

US-10-020-338-8 (1-593) x T14457 (1-150)

OY 263 ATGGGTCCGCGCAGAGTGCAGCTGAAGCGGATAGAGAACAAGATAAATCGCAGGTACC 322
|||||
Db 1 MetGIyArGGLyArGVAlGlInLeuLySArGIleGIuAnLylLSAsnArGSLnValThr 20
323 TTCTCCAAAGCGCCGCAACGGGCTCTGAAGAAAGCGCACAGATGTCCTCGTCTGTAC 382
|||||
Db 21 PheSerLySArGARserGIyLeuLeuLySLAsnIleSGLIILeserValLeuLySasp 40
OY 383 GCGAGAGTGCGCGCTATGCTGTTCTCCCCCAAAGCAAGCTTAAGTAGAGCCAC 442
|||||
Db 41 AlaGIuValSerLeuIleValPheSerHislySGLyLSLeuPheGLuTySerSerclu 60
OY 443 TCACCATGACAAAATTCTTGAACGTTATGAGCGCTACTTATGCTGAAAAGGCTTT 502
|||||

Db 61 SerGlyMetGluValLeuGlnArgTyrSerTYRAlaGlnLysIleu 80

QY 503 ATTTCAGCTGAATCT-----GAAAGTAGGGAAATTGTGCACGAAATACAGAAACTT 556
:::|||||
Db 81 LysAlaProAspSerHisValAlaSnlaGlnThrSerMetGluTyrSerArgLeu 100
|||

QY 557 AAGCGAAGATTGAG 571
|||||

Db 101 LysAlaLysIleGln 105
|||

RESULT 11
T14456
MADS box protein homolog CAL - wild cabbage
C.Species: Brassica oleracea (wild cabbage)
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C.Accession: T14456
S.Kempin, S.A.; Savidge, B.; Yanofsky, M.F.
Science 267, 522-525, 1995
A.Title: Molecular basis of the cauliflower phenotype in Arabidopsis.
A.Reference number: Z18101; MUID:95125463; PMID:7824951
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 1-251 <KMW>
A.Cross-references: EMBL:L36926; NID:G642590; PIDDN:AAA44790.1; PID:G642591
A.Experimental source: floral meristem
C.Genetics:
A.Gene: CAL
C.Superfamily: transcription factor squa; serum response factor DNA-binding domain homo
C.Keywords: DNA binding; nucleus; transcription regulation
F.2-57/Domains: serum response factor DNA-binding domain homology <SR>

Alignment Scores:

Pred. No.:	1.48e-26	Length:	251
Score:	382.00	Matches:	74
Percent Similarity:	85.32%	Conservative:	19
Best Local Similarity:	57.89%	Mismatches:	14
Query Match:	37.09%	Indels:	2
DB:	2	Gaps:	1

US-10-020-338-8 (1-593) x T14456 (1-251)

QY 263 ATGGTGCCGGCAAGTGCACCTGAAGCGGATAAGAACAAGATTAATCCGACAGTGACC 322
|||

Db 1 MetGlyArgGlyArgValGluMetLysArgIleGlnLysIleAsnArgGlnAlaThr 20
|||

QY 323 TTCGCCAAGCCCGGAAAGGGCTCCTGAAGAAGGGCGACGAGATCTCCGCTCTGTGAC 382
|||

Db 21 PheSerLysAlaGlyAlaGlyLeuLeuLysLysAlaHisGlnIleSerIleLeucynasp 40
|||

QY 383 GCGAGAGTCCGCGTATCATGTCCTTCTCCCCCAAAGGCAAGCTCTATGATACGCCACGAC 442
|||

Db 41 AlaGluValSerIleuIleValPheSerHisLysGlyLysLeuPheGlnIlyrSerSerclu 60
|||

QY 443 TCACGATGACAAATTTCTTGAACGTTATAGCGCTACTTTATGCTGAAGAGCTCTT 502
|||

Db 61 SerGlyMetGluValLeuGlnIleIleTyrgLnuArgTyrSerTYRAlaGlnLysIleu 80
|||

QY 503 ATTTCAGCTGAATCT-----GAAAGTAGGGAAATTGTGCACGAAATACAGAAACTT 556
:::|||||

Db 81 LysValProAspSerHisValAlaSnlaGlnThrSerMetGluTyrSerArgLeu 100
|||

QY 557 AAGCGAAGATTGAGACCATAAAAA 583
|||||

Db 101 LysAlaLysIleGlnLeuLeuGlnArg 109
|||

RESULT 12
T10714
MADS-box protein CMBl - clove pink
C.Species: Dianthus caryophyllus (clove pink)
C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jan-2000
C.Accession: T10714
R.Baudinette, S.C.; Savin, K.W.

OY 563 AAGATTGAGACCATACAAATGTCACAG 592
: : : : :
Db 101 ArgLeuGIuValLeuGIuArgAnGIuLys 110

RESULT 7

S23730

MADS box protein TDR4 - tomato

N/Alternate names: floral homeotic protein TM4

C/Species: Lycopersicon esculentum (tomato)

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 24-Sep-1999

C/Accession: S23730

R/Punell, L.; Abu-Abaid, M.; Zamir, D.; Nacken, W.; Schwarz-Sommer, Z.; Lifschitz, E.

Plant J. 1: 255-266, 1991

A/Title: The MADS box gene family in tomato: temporal expression during floral development

A/Reference number: S23728; MUID:93251098; PMID:1688249

A/Accession: S23730

A/Molecule type: mRNA

A/Residues: 1-227 <PNU>

A/Cross-references: EMBL:X60757; NID:g19381; PIDN:CAA43169.1; PID:g19382

A/Genetics:

A/Map position: 6

C/Superfamily: transcription factor equa; serum response factor DNA-binding domain homol

C/Keywords: DNA binding; nucleus; transcription regulation

F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Alignment Scores:
Pred. No.: 6.39e-29 Length: 227
Score: 408.00 Matches: 79
Percent Similarity: 85.45% Conservative: 15
Best Local Similarity: 71.82% Mismatches: 16
Query Match: 39.61% Indels: 0
Gaps: 0

US-10-020-338-8 (1-593) x S23730 (1-227)
OY 263 ATGGGTGCGCGCAAGTGCAGCTGAGCGGATGAGCAAGATTAATCGGAGTGACC 322
: : : : :
Db 1 MetGIyArgGIyArgValGIuLeuLysArgIleGIuAsnLysIleAsnArgGIuValThr 20

OY 323 TTCTCCAGCGCGCGCAACGGGCTCTGGAAGAGCGCAGATCTCCGCTCTGTGAC 382

Db 21 PheSerLysArgArgSerGIyLeuLeuLysLysAlaHisGIuLysSerValLeuLysAsp 40

OY 383 GCGAGGTGCGCGCTATGCTCTTCTCCCAAGGCAAGCTTATGATGACGCCACGAC 442

Db 41 AlaGIuValGIyLeuLysLeuValPheSerThrLysGIyLysLeuPheGIuLysAlaAsnAsp 60

OY 443 TCCAGCATGACAAATTTCTTGAACGTTATGAGCGCTCTTATGCTGAAAGGCTTT 502

Db 61 SerCysMetGIuArgIleLeuGIuArgIyGIuValGlySerPheAlaGIuLysGIuLeu 80

OY 503 ATTTACAGTGAATCTGAAAGTGAAGGAATGTGTCCGCAATACAGAACTTAAGCGC 562

Db 81 ValProThrAspHisThrSerProValSerThrPheLeuGIuHisArgLysLeuLysAla 100

OY 563 AAGATTGAGACCATACAAATGTCACAG 592

Db 101 ArgLeuGIuValLeuGIuArgAnGIuLys 110

RESULT 8

T07100

MADS box protein homolog POTM1-1 - potato

C/Species: Solanum tuberosum (potato)

C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000

C/Accession: T07100

R/Kang, S.G.; Hannapel, D.J.

Gene 166, 329-330, 1995

A/Title: Nucleotide sequences of novel potato (Solanum tuberosum L.) MADS-box cDNAs and

A/Reference number: Z15919; MUID:96125213; PMID:8543185

A/Accession: T07100

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-250 <KAN>

A/Cross-references: EMBL:U23757; NID:g758564; PIDN:AAA92839.1; PID:g758565

A/Experimental source: cv. Superior; vegetative tissue; tuber induced 4-day axillary bu

C/Genetics:

A/Gene: POTM1-1

C/Function:

A/Description: may be involved in vegetative organ development of potato

C/Superfamily: transcription factor equa; serum response factor DNA-binding domain homo

C/Keywords: DNA binding; nucleus; transcription factor; transcription regulation

F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Alignment Scores:

Pred. No.: 9.84e-29 Length: 250
Score: 406.00 Matches: 77
Percent Similarity: 85.45% Conservative: 17
Best Local Similarity: 70.00% Mismatches: 16
Query Match: 39.42% Indels: 0
Gaps: 0

US-10-020-338-8 (1-593) x T07100 (1-250)

OY 263 ATGGGTGCGCGCAAGTGCAGCTGAGCGGATGAGCAAGATTAATCGGAGTGACC 322

Db 1 MetGIyArgGIyArgValGIuLeuLysArgIleGIuAsnLysIleAsnArgGIuValThr 20

OY 323 TTCTCCAGCGCGCGCAACGGGCTCTGGAAGAGCGCAGATCTCCGCTCTGTGAC 382

Db 21 PheSerLysArgArgSerGIyLeuLeuLysLysAlaHisGIuLysSerValLeuLysAsp 40

OY 383 GCGAGGTGCGCGCTATGCTCTTCTCCCAAGGCAAGCTTATGATGACGCCACGAC 442

Db 41 AlaGIuValGIyLeuLysLeuValPheSerThrLysGIyLysLeuPheGIuLysAlaAsnAsp 60

OY 443 TCCAGCATGACAAATTTCTTGAACGTTATGAGCGCTCTTATGCTGAAAGGCTTT 502

Db 61 SerCysMetGIuArgIleLeuGIuArgIyGIuValGlySerPheAlaGIuLysGIuLeu 80

OY 503 ATTTACAGTGAATCTGAAAGTGAAGGAATGTGTCCGCAATACAGAACTTAAGCGC 562

Db 81 ValProThrAspHisThrSerProValSerThrPheLeuGIuHisAlaLysLeuLysAla 100

OY 563 AAGATTGAGACCATACAAATGTCACAG 592

Db 101 ArgLeuGIuValLeuGIuArgAnGIuLys 110

RESULT 9

S71208

MADS box protein AGL8 - Arabidopsis thaliana

N/Alternate names: agamous-like protein 8

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 24-Sep-1999

C/Accession: S71208

R/Mandel, M.A.; Yanofsky, M.F.

Submitted to the EMBL Data Library, August 1995

A/Description: The Arabidopsis AGL8 MADS box gene is expressed in inflorescence meriste

A/Reference number: S71208

A/Accession: S71208

A/Molecule type: mRNA

A/Residues: 1-242 <MAN>

A/Cross-references: EMBL:U34473; NID:g1004364; PIDN:AAA97403.1; PID:g1004365

C/Genetics:

A/Gene: AGL8

C/Superfamily: transcription factor equa; serum response factor DNA-binding domain homo

C/Keywords: DNA binding; nucleus; transcription regulation

F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Alignment Scores:

Pred. No.: 4.22e-28 Length: 242
Score: 399.00 Matches: 75
Percent Similarity: 85.98% Conservative: 17
Best Local Similarity: 70.09% Mismatches: 15
Query Match: 38.74% Indels: 0

Pred. No.: 2.3e-30 Length: 254
Score: 424.00 Matches: 82
Percent Similarity: 88.79% Conservative: 13
Best Local Similarity: 76.64% Mismatches: 12
Query Match: 41.17% Indels: 0
DB: 2 Gaps: 0

US-10-020-338-8 (1-593) x S52236 (1-254)

QY 263 ATGGGTCGCGCAAGTGCAGCTGAGGAGGATAGAGAACAGATAATTCGGCAGGTGACC 322
Db 1 MetGlyArgGlyArgValGlnLeuLysArgIleGluLeuLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAAAGCGCGCAACGGGCTCCTGAAGAGGCGCAGAGATCTCCGCTCTGTGAC 382
Db 21 PheSerLysArgGlyArgValGlnLeuLysLysIleGluIleSerValLeuLysAsp 40
QY 383 GCGGAGGTCCGCGTATGCTCTTCTCCCAAGGCAAGCTCTATGATGACCCAGC 442
Db 41 AlaGluValAlaLeuValValPheSerHisLysGlyLysLeuPheGluLysSerThrAsp 60
QY 443 TCCAGCATGAGCAAAATTTCTGAACGTTATGAGCGCTCTATGCTGAAGAGGCTCTT 502
Db 61 SerCysMetGluLysIleLeuGluArgTyrGluArgTyrSerTyrAlaGluArgGlnLeu 80
QY 503 ATTTCAGCTGAATCTGAAGAGGAGAAATTGGTCCACGATACAGAGAACTTAAGCG 562
Db 81 IleAlaProGluSerAspValAsnThrAsnTrpSerMetGluTyrAsnArgLeuLysAla 100
QY 563 AAGATTGAGACCATCAAAAA 583
Db 101 LysIleGluLeuLeuGluArg 107

RESULT 5

S27109

MADS box protein API - Arabidopsis thaliana

N/Alternate names: Floral homeotic protein API

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 24-Sep-1999

C/Accession: S27109; S36597

R/Mandel, M.A.; Gustafson-Brown, C.; Savidge, B.; Yanofsky, M.F.

Nature 360, 273-277, 1992

A/Title: Molecular characterization of the Arabidopsis floral homeotic gene APETAL1.

A/Reference number: S27109; MUID:93063372; PMID:1359429

A/Accession: S27109

A/Molecule type: mRNA

A/Residues: 1-256 <MAN>

A/Cross-references: EMBL:Z16421; NID:g16161; PIDN:CAA78909.1; PID:g16162

Note: 27-Asp was also found

Yanofsky, M.F.

Submitted to the EMBL Data Library, October 1992

A/Reference number: S36597

A/Accession: S36597

A/Molecule type: mRNA

A/Residues: 1-235,237-256 <YAN>

A/Cross-references: EMBL:Z16421; NID:g16161; PIDN:CAA78909.1; PID:g16162

C/Genetics:

A/Map position: 1

C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

C/Keywords: DNA binding; nucleus; transcription regulation

F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Alignment Scores:

Pred. No.: 2.31e-30 Length: 256
Score: 424.00 Matches: 82
Percent Similarity: 88.79% Conservative: 13
Best Local Similarity: 76.64% Mismatches: 12
Query Match: 41.17% Indels: 0
DB: 2 Gaps: 0

US-10-020-338-8 (1-593) x S27109 (1-256)

QY 263 ATGGGTCGCGCAAGTGCAGCTGAGGAGGATAGAGAACAGATAATTCGGCAGGTGACC 322

Db 1 MetGlyArgGlyArgValGlnLeuLysArgIleGluLeuLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAAAGCGCGCAACGGGCTCCTGAAGAGGCGCAGAGATCTCCGCTCTGTGAC 382
Db 21 PheSerLysArgGlyArgValGlnLeuLysLysIleGluIleSerValLeuLysAsp 40
QY 383 GCGGAGGTCCGCGTATGCTCTTCTCCCAAGGCAAGCTCTATGATGACCCAGC 442
Db 41 AlaGluValAlaLeuValValPheSerHisLysGlyLysLeuPheGluLysSerThrAsp 60
QY 443 TCCAGCATGAGCAAAATTTCTGAACGTTATGAGCGCTCTATGCTGAAGAGGCTCTT 502
Db 61 SerCysMetGluLysIleLeuGluArgTyrGluArgTyrSerTyrAlaGluArgGlnLeu 80
QY 503 ATTTCAGCTGAATCTGAAGAGGAGAAATTGGTCCACGATACAGAGAACTTAAGCG 562
Db 81 IleAlaProGluSerAspValAsnThrAsnTrpSerMetGluTyrAsnArgLeuLysAla 100
QY 563 AAGATTGAGACCATCAAAAA 583
Db 101 LysIleGluLeuLeuGluArg 107

RESULT 6

T07902

MADS box protein - Commerson's wild potato

C/Species: Solanum commersonii (Commerson's wild potato)

C/Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 08-Oct-1999

C/Accession: T07902

R/Seppanen, M.M.

Submitted to the EMBL Data Library, May 1997

A/Description: Nucleotide sequence of novel wild potato (Solanum commersonii) MADS-box

A/Reference number: Z16201

A/Accession: T07902

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-250 <SBP>

A/Cross-references: EMBL:AF002666; NID:g2290777; PIDN:AAB65161.1; PID:g2290778

C/Genetics:

A/Gene: SCML

C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homo

C/Keywords: DNA binding; nucleus; transcription regulation

F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Alignment Scores:

Pred. No.: 4.27e-29 Length: 250
Score: 410.00 Matches: 79
Percent Similarity: 85.45% Conservative: 15
Best Local Similarity: 71.82% Mismatches: 16
Query Match: 39.81% Indels: 0
DB: 2 Gaps: 0

US-10-020-338-8 (1-593) x T07902 (1-250)

QY 263 ATGGGTCGCGCAAGTGCAGCTGAGGAGGATAGAGAACAGATAATTCGGCAGGTGACC 322
Db 1 MetGlyArgGlyArgValGlnLeuLysArgIleGluLeuLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAAAGCGCGCAACGGGCTCCTGAAGAGGCGCAGAGATCTCCGCTCTGTGAC 382
Db 21 PheSerLysArgGlyArgValGlnLeuLysLysIleGluIleSerValLeuLysAsp 40
QY 383 GCGGAGGTCCGCGTATGCTCTTCTCCCAAGGCAAGCTCTATGATGACCCAGC 442
Db 41 AlaGluValAlaLeuValValPheSerHisLysGlyLysLeuPheGluLysSerThrAsp 60
QY 443 TCCAGCATGAGCAAAATTTCTGAACGTTATGAGCGCTCTATGCTGAAGAGGCTCTT 502
Db 61 SerCysMetGluLysIleLeuGluArgTyrGluArgTyrSerTyrAlaGluArgGlnLeu 80
QY 503 ATTTCAGCTGAATCTGAAGAGGAGAAATTGGTCCACGATACAGAGAACTTAAGCG 562
Db 81 ValProThrAspHisThrSerProGluLysSerTyrPheLeuGluLeuAlaLysLeuLysAla 100

OY 383 GCGAGAGTCGCGATGCTCTTCCCGCAAGGCAAGCTTATGATGACCGCAGC 442
 Db 41 AlagluvalalavalillevaPheSerProlysglylsuylrGluTyrAlaThrAsp 60
 OY 443 TCCAGCATGGAACAATTTCTGAACGTTATGAGCGCTACTCTTGTGTAAGAGCTCTT 502
 Db 61 SerArgMetAspIlystleuGluArgTyrGluArgTyrSerTyrAlaGluLysAlaIleu 80
 OY 503 ATTTCAGCTGAATCTGAAGAGGAAATTTGTCGCCAGATACAGAACTTAAAGCG 562
 Db 81 lIeSerlAgIuSerGluSerGluGlyAsnTrpCyshIsgIuTyrArgLysleuLysAla 100
 OY 563 AAGATTGAGACCATACAAAATGTCACAAG 592
 Db 101 LysIleGluIuTrlIleGluLysCyshIlys 110

RESULT 2

MADS box protein - sorghum (fragment)
 Species: Sorghum bicolor (sorghum)
 Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000

C/Accession: T14737
 R/Greco, R.; Steagl, L.; Colombo, L.; Angenent, G.C.; Sari-Gorla, M.; Pe, M.E.
 Mol. Gen. Genet. 253, 615-623, 1997
 A/Title: MADS box genes expressed in developing inflorescences of rice and sorghum.
 A/Reference number: Z15292; MUID:97218034; PMID:9065695
 A/Accession: T14737
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-228 <GRE>
 A/Cross-references: EMBL:U32110; NID:G1905933; PIDN:AA50181.1; PID:G1905934
 C/Genetics:
 A/Gene: MADS2
 C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
 C/Keywords: DNA binding; nucleus; transcription regulation

Alignment Scores:

Pred. No.:	8 53e-41	Length:	228
Score:	539.00	Matches:	105
Percent Similarity:	99.06%	Conservative:	0
Best Local Similarity:	99.06%	Mismatches:	1
Query Match:	52.33%	Indels:	0
DB:	2	Gaps:	0

US-10-020-338-8 (1-593) x T14737 (1-228)

OY 275 AAGGTGACGTGAAGCGGATAGAGAACAATTCGACGTCACCTTCTCCAGGCG 334
 Db 1 LysValGlnLeuLysArgIleGluAsnLysIleAsnArgGlnValThrPheSerLysArg 20
 OY 335 CGCAACGGGCTCTGGAAGAGCGCAGAGATCTCCGTCCTGTGACGGAGGTCGCC 394
 Db 21 ArgAsnGlyLeuLeuLysAlaHisGluIleSerValIleuCyAspAlaGluValAla 40
 OY 395 GTCATCGCTCTCCCGCAAGGCAAGCTATGATGTCGCGACCGATCCAGCATGAGC 454
 Db 41 ValIleValPheSerProlysglylsuylrGluTyrAlaThrAspSerArgMetAsp 60
 OY 455 AAAATTTCTGAACGTTATGAGCGCTACTCTTATGCTGAAGAGCTTATTTCAAGCTGA 514
 Db 61 LysIleleuGluArgTyrGluArgTyrSerTyrAlaGluLysAlaIleSerIleGlu 80
 OY 515 TCTGAAAGTGAAGGAAATTTGTCGCCAGATACAGAACTTAAAGCGAGATTGAGAC 574
 Db 81 SerGluSerGluGlyAsnTrpCyshIsgIuTyrArgLysleuLysAlaIleGluThr 100
 OY 575 ATACAAAATGTCACAAG 592
 Db 101 lIleGluLysCyshIlys 106

RESULT 3

S20886
 MADS box protein squa - garden snapdragon

N/Alternate names: transcription factor, squa
 C/Species: Antirrhinum majus (garden snapdragon)
 C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 24-Sep-1999
 C/Accession: S20886
 R/Hilfser, P.; Klein, J.; Loening, W.E.; Meijer, H.; Saedler, H.; Sommer, H.
 EMBO J. 11, 1239-1249, 1992
 A/Title: Bracteomania, an inflorescence anomaly, is caused by the loss of function of t
 A/Reference number: S20886; MUID:92224862; PMID:1563342
 A/Accession: S20886
 A/Molecule type: DNA
 A/Residues: 1-248 <HUI>
 A/Cross-references: EMBL:X63701; NID:G16051; PIDN:CAA45228.1; PID:G16052
 C/Genetics:
 A/Gene: squa
 A/Insertions: 62/2; 88/3; 110/2; 143/3; 157/3; 171/3; 215/2
 C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homo
 C/Keywords: DNA binding; nucleus; transcription regulation
 F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Alignment Scores:

Pred. No.:	3.51e-31	Length:	248
Score:	433.00	Matches:	83
Percent Similarity:	88.18%	Conservative:	14
Best Local Similarity:	75.45%	Mismatches:	13
Query Match:	42.04%	Indels:	0
DB:	2	Gaps:	0

US-10-020-338-8 (1-593) x S20886 (1-248)

OY 263 ATGGGTGCGCGCAAGTGCAGTGAAGCGGATAGAGAACAATTCGACGTCAGTACC 322
 Db 1 MetCylArgGlyIysValGlnLeuLysArgIleGluAsnLysIleAsnArgGlnValThr 20
 OY 323 TTCTCCAGCGCGCAACGAGCTCTCTGAAGAGCGCAGAGATCTCCGTCCTGTGAC 382
 Db 21 PheSerLysArgArgGlyIleuLeuLysAlaHisGluIleuSerValIleuCyAsp 40
 OY 383 GCGAGAGTCGCGCATCGCTCTCCCGCAAGGCAAGCTATGATGTCGCGACCGAC 442
 Db 41 AlagluvalalavalillevaPheSerAsnLysleuPheGluTyrSerThrAsp 60
 OY 443 TCCAGCATGGAACAATTTCTGAACGTTATGAGCGCTACTCTTATGCTGAAGAGCTCTT 502
 Db 61 SerCysMetAspArgIleleuGluLysTyrGluArgTyrSerPheAlaGluArgGlnLeu 80
 OY 503 ATTTCAGCTGAATCTGAAGAGGAAATTTGTCGCCAGATACAGAACTTAAAGCGC 562
 Db 81 ValSerAsnGluProGlnSerProAlaAsnTrpThrLeuGluTyrSerLysleuLysAla 100
 OY 563 AAGATTGAGACCATACAAAATGTCACAAG 592
 Db 101 ArgIleGluLeuLeuGlnArgAsnHisArg 110

RESULT 4

S52236
 MADS box protein ap1 - white mustard

N/Alternate names: floral homeotic protein ap1
 C/Species: Sinapis alba (white mustard)
 C/Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 24-Sep-1999
 C/Accession: S52236
 R/Menzel, G.; Apel, K.; Meijer, S.
 submitted to the EMBL Data Library, September 1994
 A/Description: Isolation and sequencing of the mustard (Sinapis alba L.) ap1 cDNA.
 A/Reference number: S52236
 A/Accession: S52236
 A/Molecule type: mRNA
 A/Residues: 1-254 <MEN>
 A/Cross-references: EMBL:X81480; NID:G609252; PIDN:CAA57233.1; PID:G609253
 C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homo
 C/Keywords: DNA binding; nucleus; transcription regulation
 F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Alignment Scores:

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: June 24, 2003, 14:06:08 ; Search time 24 Seconds
(without alignments)
4750.643 Million cell updates/sec

Title: US-10-020-338-8

Perfect score: 1030
Sequence: 1 cccgctgcaccacgctccg.....catcaaaaatgtcacagc 593

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Xgapop 10.0 , Xgapext 0.5
Xgapop 6.0 , Xgapext 7.0
Delop 6.0 , Delext 7.0

Archived: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 566448

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-O=/cgm2/1/USPTO.spool/US10020338/runat_24062003_102355_21519/app_query.fasta.1.775
-DB=PIR_73 -QFMT=fasten -SUPFIX=rpt -MINMATCH=0.1 -IOFCL=0 -IOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10020338 @CGN 1.1 62 @runat_24062003_102355_21519 -NCPU=6 -ICPU=3
-NO MMAP -LARGEOUTRY -NEG.SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -MARK.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	561	54.5	273	2	T03410
2	539	52.3	228	2	T14737
3	433	42.0	248	2	S20886
4	424	41.2	254	2	S52236
5	424	41.2	256	2	S27109
6	410	39.8	250	2	T07902
7	408	39.6	227	2	S23730
8	406	39.4	250	2	T07100
9	399	38.7	242	2	S71208
10	386	37.5	150	2	T14457
11	382	37.1	251	2	T14456
12	353.5	34.3	233	2	T10714
13	352.5	34.2	261	2	S51935
14	352.5	34.2	261	2	T09603

15	345	33.5	249	2	T04307	M79 protein - rice
16	342	33.2	249	2	T04335	MADS box protein -
17	340	33.0	248	2	T04170	MADS box protein -
18	340	33.0	259	2	T04169	MADS box protein -
19	333	32.3	231	2	T14801	MADS box protein M
20	330.5	32.1	224	2	T01690	MADS box protein F
21	330	32.0	250	2	T04167	MADS box protein -
22	329	31.9	242	2	T10486	MADS box protein -
23	329	31.9	242	2	T09571	MADS box protein M
24	327.5	31.8	245	2	T09569	MADS box protein M
25	327	31.7	247	2	S78015	MADS box protein D
26	326.5	31.7	247	2	T06543	MADS box protein -
27	325	31.6	246	2	T17023	MADS box protein I
28	322.5	31.3	255	2	T03408	MADS box protein -
29	322	31.3	248	2	B39534	MADS box protein A
30	322	31.3	250	2	D39534	MADS box protein A
31	322	31.3	262	2	T51409	MADS box protein A
32	321	31.2	243	2	S71756	MADS box protein D
33	319.5	31.0	224	2	S23728	MADS box protein T
34	318	30.9	255	2	T03398	MADS box protein -
35	317.5	30.8	242	2	S71757	MADS box protein D
36	315.5	30.6	254	2	T10467	MADS box protein D
37	314.5	30.5	251	2	T00656	MADS box protein A
38	313.5	30.4	225	2	T04168	MADS box protein -
39	308.5	30.0	250	2	S40405	MADS box protein -
40	307.5	29.9	257	2	S53306	MADS box protein M
41	305	29.6	252	2	F39534	floral homeotic pr
42	301.5	29.3	234	2	A84515	probable MADS-box
43	301.5	29.3	234	2	T52100	MADS-box transcrip
44	300	29.1	258	2	S57793	MADS box protein A
45	282	27.4	60	2	S55938	MADS box protein Z

ALIGNMENTS

RESULT 1
T03410
MADS box protein - maize
C:Species: Zea mays (maize)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Sep-1999
C:Accession: T03410
R:Mena, M.; Mandel, M.A.; Lerner, D.R.; Yanofsky, M.F.; Schmidt, R.J.
Plant J. 8, 845-854, 1995
A:Title: A characterization of the MADS-box gene family in maize.
A:Reference number: Z14928; MUID:96132144; PMID:8580958
A:Accession: T03410
A:Status: preliminary; translated from GE/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-273 <MEN>
A:Cross-references: EMBL:L46400; NID:9939784; PIDN:AAB00081.1; PID:9939785
C:Genetics:
A:Note: ZAP1
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homo
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Alignment Scores:

Pred. No.: 8.9e-43
Score: 561.00
Percent Similarity: 99.09%
Best Local Similarity: 99.09%
Query Match: 54.47%
DB: 2
Gaps: 0

US-10-020-338-8 (1-593) x T03410 (1-273)

Oy	263	ATGGGTCGCGCAAGGTGACGCTGACGATAGACAAGCATTAATCGGACGTGAC	322
Db	1	MctcllyarvgilyValGlnleulyaRglleglunhnySllAenAaRgGlnValThr	20
Oy	323	TTTCTCAAGGCGCCGCAACGGGCTCTCTGAAGAAGCGGACGAGATCTCCGTCGTGAC	382
Db	21	PheserlysarYarGaengilyLeuLeulySylahistgiuileSerValLeucyasp	40

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Db 101 ArgTYrGIuAsnLeuGlnArg 107

RESULT 14

US-09-853-450-30

Sequence 30, Application US/09853450

Publication No. US20020194645A1

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.

APPLICANT: Pelaz, Soraya

APPLICANT: Ditta, Gary

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Exhibiting Modulated Reproductive Development

FILE REFERENCE: 19452A-002400US

CURRENT FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 61

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 30

LENGTH: 250

TYPE: PRT

ORGANISM: Arabidopsis thaliana

FEATURE:

OTHER INFORMATION: SEPALLATA2 (SEP2)

US-09-853-450-30

Alignment Scores:

Pred. No.:	5,95e-23	Length:	250
Score:	322.00	Matches:	64
Percent Similarity:	78.50%	Conservative:	20
Best Local Similarity:	59.81%	Mismatches:	23
Query Match:	31.26%	Indels:	0
DB:	9	Gaps:	0

US-10-020-338-8 (1-593) x US-09-853-450-30 (1-250)

QY 263 ATGGTCGGCGGCAAGTGCAGCTGAAGCGGATGAGAACAGATAATCGCGAGTGACC 322

Db 1 MetGlyArgGlyArgValGluLeuLysArgIleGluAsnLysIleAsnArgGlnValThr 20

QY 323 TTCTCCAAAGCGCGCAAGCGGCTCCTGAAGAGCGCAAGATCTCGTCTGTGAC 382

Db 21 PheAlaLysArgArgAsnGlyLeuLeuLysLysAlaTyrgluLeuSerValLeuCyasp 40

QY 383 GCGAGGTGCGCGTATGCTCTTCTCCCGCAAGGCAAGCTATAGTACCGCAC 442

Db 41 AlaGluValSerLeuLeuValPheSerAsnArgGlyLysLeuTyrgluLeuPheCyserThr 60

QY 443 TCCAGCATGACAAATTTCTTGAAGCTTATGAGCGCTACTTTATGCTGAAAAAGCTTT 502

Db 61 SerAsnMetLeuLysThrLeuGluArgTyrgluLysCyserTyrglySerIleGluVal 80

QY 503 ATTTCAGCTGAATCTGAAGTGAAGGAATTTGTCGACGAATACAGAACTTAAGCG 562

Db 81 AsnAsnLysProAlaLysGluLeuGluAsnSerTyrgluLysLeuLysGly 100

QY 563 AAGATTGAGACCAACAAA 583

Db 101 ArgTYrGIuAsnLeuGlnArg 107

RESULT 15

US-09-853-450-32

Sequence 32, Application US/09853450

Publication No. US20020194645A1

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.

APPLICANT: Pelaz, Soraya

APPLICANT: Ditta, Gary

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants

FILE REFERENCE: 19452A-002400US

CURRENT APPLICATION NUMBER: US/09/853,450

CURRENT FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 61

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 32

LENGTH: 237

TYPE: PRT

ORGANISM: Arabidopsis thaliana

FEATURE:

OTHER INFORMATION: SEPALLATA3 (SEP3)

US-09-853-450-32

Alignment Scores:

Pred. No.:	3.15e-22	Length:	237
Score:	314.50	Matches:	63
Percent Similarity:	73.50%	Conservative:	23
Best Local Similarity:	53.85%	Mismatches:	20
Query Match:	30.53%	Indels:	11
DB:	9	Gaps:	2

US-10-020-338-8 (1-593) x US-09-853-450-32 (1-237)

QY 263 ATGGTCGGCGGCAAGTGCAGCTGAAGCGGATGAGAACAGATAATCGCGAGTGACC 322

Db 1 MetGlyArgGlyArgValGluLeuLysArgIleGluAsnLysIleAsnArgGlnValThr 20

QY 323 TTCTCCAAAGCGCGCAAGCGGCTCCTGAAGAGCGCAAGATCTCGTCTGTGAC 382

Db 21 PheAlaLysArgArgAsnGlyLeuLeuLysLysAlaTyrgluLeuSerValLeuCyasp 40

QY 383 GCGAGGTGCGCGTATGCTCTTCTCCCGCAAGGCAAGCTATAGTACCGCAC 442

Db 41 AlaGluValAlaLeuIleIlePheSerAsnArgGlyLysLeuTyrgluLeuPheCyserSer 60

QY 443 TCCAGCATGACAAATTTCTTGAAGCTTATGAGCGCTACTTTATGCTGAAAAAGCTTT 490

Db 61 SerSerMetLeuArgThrLeuLysArgTyrgluLysCyserTyrglyAlaProGluPro 80

QY 491 -----GAAAGCTCTTATTTTACAGCTGAATCTGAAGTGAAGGAATTTGTCGCAC 541

Db 81 AsnValProSerArgGluAlaLeuAlaValGluLeuSerSerGln-----Gln 96

QY 542 GAATCAGAGAACTTAAGCGCAAGTTGAGACCATCAAAAATGTCACAAAG 592

Db 97 GluTyrgluLysLeuLysGluArgTyrgluAspAlaLeuGlnArgThrGlnArg 113

Search completed: June 24, 2003, 14:14:27

Job time : 31.5 secs

Score: 386.00 Matches: 75
Percent Similarity: 87.62% Conservative: 17
Best Local Similarity: 72.43% Mismatches: 11
Query Match: 37.48% Indels: 2
Gaps: 1

US-10-020-338-8 (1-593) x US-09-853-450-14 (1-150)

QY 263 ATGGGTCCGGCGAGGTGCACTGTAAGCGGATAGAGACAAATGATCGGCGAGTACC 322
DB 1 MetGlyArgGlyArgValGluMetLysArgIleGluAsnLysIleAsnArgIleValThr 20
QY 323 TTCTCCAAAGCGCGCAAGCGGCTCTGGAAGCGCGCAGAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgIleGluLeuLysLysAlaHisGluIleSerLysLeuGlyAsp 40
QY 383 GCGAGGTGCGCGTCACTGCTCTTCTCCCAAGGCAAGCCTCATGATGACGCAACGAC 442
DB 41 AlaGluValSerLeuIleValPheSerHisLysGlyLysLeuPheGluIlyrSerSerGlu 60
QY 443 TCCAGCATGACAAATTTCTTGAAGCTTATGAGCGCTACTTATCTGAAAAGCTCTT 502
DB 61 SerCysMetGluLysValLeuGluArgIlyrGluArgIlyrSerIlyrAlaGluLysGluLeu 80
QY 503 ATTTCAGCTGAATCT-----GAAAGTGAGGAAATTGGTCCACGATACAGAAACTT 556
DB 81 LysAlaProAspSerHisValAsnAlaGlnThrAsnTrpSerMetGluIlyrSerArgLeu 100
QY 557 AAGCGAGATGTGAG 571
DB 101 LysAlaLysIleGlu 105

RESULT 12

US-09-853-450-12
Sequence 12, Application US/09853450
Publication No. US20020194645A1
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Pelaz, Soraya
APPLICANT: Ditta, Gary
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
FILE REFERENCE: 19452A-002400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12

LENGTH: 251
TYPE: PRT
ORGANISM: Brassica oleracea
FEATURE:
OTHER INFORMATION: CAULIFLOWER (CAL)
US-09-853-450-12

Alignment Scores:
Pred. No.: 8.6e-29 Length: 251
Score: 382.00 Matches: 74
Percent Similarity: 85.32% Conservative: 19
Best Local Similarity: 67.89% Mismatches: 14
Query Match: 37.09% Indels: 2
Gaps: 1

US-10-020-338-8 (1-593) x US-09-853-450-12 (1-251)

QY 263 ATGGGTCCGGCGAGGTGCACTGTAAGCGGATAGAGACAAATGATCGGCGAGTACC 322
DB 1 MetGlyArgGlyArgValGluMetLysArgIleGluAsnLysIleAsnArgIleValThr 20
QY 323 TTCTCCAAAGCGCGCAAGCGGCTCTGGAAGCGCGCAGAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgIleGluLeuLysLysAlaHisGluIleSerLysLeuGlyAsp 40

QY 383 GCGAGGTGCGCGTCACTGCTCTTCTCCCAAGGCAAGCCTCATGATGACGCAACGAC 442
DB 41 AlaGluValSerLeuIleValPheSerHisLysGlyLysLeuPheGluIlyrSerSerGlu 60
QY 443 TCCAGCATGACAAATTTCTTGAAGCTTATGAGCGCTACTTATGCTGAAAAGCTCTT 502
DB 61 SerCysMetGluLysValLeuGluHisIlyrGluArgIlyrSerIlyrAlaGluLysGluLeu 80
QY 503 ATTTCAGCTGAATCT-----GAAAGTGAGGAAATTGGTCCACGATACAGAAACTT 556
DB 81 LysValProAspSerHisValAsnAlaGlnThrAsnTrpSerValGluIlyrSerArgLeu 100
QY 557 AAGCGAGATGTGACATCAAAAA 583
DB 101 LysAlaLysIleGluLeuGluArg 109

RESULT 13

US-09-853-450-28
Sequence 28, Application US/09853450
Publication No. US20020194645A1
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Pelaz, Soraya
APPLICANT: Ditta, Gary
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
FILE REFERENCE: 19452A-002400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 248
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: SEPALLATA1 (SEPL1)
US-09-853-450-28

Alignment Scores:
Pred. No.: 5.94e-23 Length: 248
Score: 322.00 Matches: 63
Percent Similarity: 78.50% Conservative: 21
Best Local Similarity: 58.88% Mismatches: 23
Query Match: 31.26% Indels: 0
Gaps: 0

US-10-020-338-8 (1-593) x US-09-853-450-28 (1-248)

QY 263 ATGGGTCCGGCGAGGTGCACTGTAAGCGGATAGAGACAAATGATCGGCGAGTACC 322
DB 1 MetGlyArgGlyArgValGluMetLysArgIleGluAsnLysIleAsnArgIleValThr 20
QY 323 TTCTCCAAAGCGCGCAAGCGGCTCTGGAAGCGCGCAGAGATCTCCGCTCTGTGAC 382
DB 21 PheAlaLysArgArgAsnGlyLeuLeuLysLysAlaIlyrGluLeuSerValLeuGlyAsp 40
QY 383 GCGAGGTGCGCGTCACTGCTTCTCCCAAGGCAAGCCTCATGATGACGCAACGAC 442
DB 41 AlaGluValAlaLeuIleIlePheSerAsnArgIlyrLysLeuIlyrGluPheCysSerSer 60
QY 443 TCCAGCATGACAAATTTCTTGAAGCTTATGAGCGCTACTTATGCTGAAAAGCTCTT 502
DB 61 SerAsnMetLeuIlyrThrLeuAspArgIlyrGluLysCysSerIlyrGlySerIleGluVal 80
QY 503 ATTTCAGCTGAATCTGGAAGTGAAGAAATTGCTCCACGATACAGAAACTTAAGCG 562
DB 81 AsnAsnLysProAlaLysGluLeuGluLysSerIlyrArgGluIlyrLeuLysLeuGly 100
QY 563 AAGATTGAGACCATCAAAAA 583
DB 101 LysAlaLysIleGluLeuGluArg 109

	Db	101 ArgValGluValLeuGlnIuylus 107		
RESULT 9				
US-09-978-730-2				
Sequence 2, Application US/09978730				
Patent No. US20020129403A1				
GENERAL INFORMATION:				
APPLICANT: Yanoofsky, Martin F.				
APPLICANT: Liljegen, Sarah				
TITLE OF INVENTION: The Regents of the University of California				
TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic				
FILE REFERENCE: 19452A-000920US				
CURRENT APPLICATION NUMBER: US/09/978,730				
CURRENT FILING DATE: 2001-10-15				
PRIOR APPLICATION NUMBER: US 60/090,649				
PRIOR FILING DATE: 1998-06-25				
PRIOR APPLICATION NUMBER: US 09/339,998				
PRIOR FILING DATE: 1999-06-25				
NUMBER OF SEQ ID NOS: 25				
SOFTWARE: PatentIn Ver. 2.1				
SEQ ID NO 2				
LENGTH: 242				
TYPE: PRT				
ORGANISM: Arabidopsis sp.				
US-09-978-730-2				
Alignment Scores:				
Pred. No.: 1.89e-30			Length: 242	
Score: 399.00			Matches: 75	
Percent Similarity: 85.98%			Conservative: 17	
Best Local Similarity: 70.09%			Mismatches: 15	
Query Match: 38.74%			Indels: 0	
DB: 10			Gaps: 0	
US-10-020-338-8 (1-593) x US-09-978-730-2 (1-242)				
OY	263	ATGGGTGCGCGCAAGTGCAGCTGAAGCGGATAGAACAACAGATAATTCGCGAGTGACC	3222	
Db	1	MeGclYArgrlYArglYValGlneulYsArglleGIuaenlylEasArGrGlnValThr	20	
OY	323	TTTCTCCAAAGGCCGCAACGGCCTCCCTGAAGAGCGGACAGAGATTCCGTCTCTGTGAC	382	
Db	21	PheserlysrArgrlsrGerlgyleuleulYslYsAlahSgullEservValleucYAsp	40	
OY	383	GCGGAGGTCCGCTCATGCTCTCTCTCCGCCAAAGCGCAAGCTCTATGACTAGCCACCGAC	442	
Db	41	AlagluValalaleuileValpheserSerlySglYslbleuPhedglutYserThrasp	60	
OY	443	TCCAGCATGCAAAAATTTCTTGAAAGCTTAATVYAGCGCTACTCTTATGCTGAAAAAGCTCTT	502	
Db	61	SercyweclwrlarglleuenglurgtYrAspargtYrleuYserAsplyGlnleu	80	
OY	503	ATTTCACGCTGAATCTGAAGTAGGGAATTGTGCGCAAGTAATACAGAACTTAAGCG	562	
Db	81	ValGlyArgrsArplserGlnserGlnuAntPrValleuGlnHsalatYsleuYsAla	1000	
OY	563	AAGATTGAGCACATACAAA 583		
Db	101	ArgValGluValLeuGlnIuylus 107		
RESULT 10				
US-09-853-450-10				
Sequence 10, Application US/09853450				
Publication No. US20020194645A1				
GENERAL INFORMATION:				
APPLICANT: Yanoofsky, Martin F.				
APPLICANT: Pelaz, Soraya				
APPLICANT: Ditta, Gary				
TITLE OF INVENTION: The Regents of the University of California				
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants				
TITLE OF INVENTION: Exhibiting Modulated Reproductive Development				

```

FILE REFERENCE : 19452A-002400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 10
LENGTH: 255
TYPE: PRF
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: CAULIFLOWER (CAL)
US-09-853-450-10.

Alignment Scores:
Pred. No.:          9,18e-30          Length:          255
Score:              392.00            Matches:          76
Percent Similarity: 87.16%            Conservative:     19
Best Local Similarity: 69.72%          Mismatches:      12
Query Match:        38.06%            Indels:         2
DB:                  9                Gaps:            1

US-10-020-338-8 (1-593) x US-09-853-450-10 (1-255)

QY      263  ATGGATCGCGGCGAGGTGCAGCTGAGGCGGATAGCAACAAGATAATTCGCGAGGTGACC 322
Db      1  MGGIYARGIGLYARGVALGILNENLYSARGILLEGILNENLYSILEAHNARGINVALThr 20

QY      323  TTCTCCAAAGCGCGCGCAACGGGCTCTGTGAAGAGGCGCAGGATCTCCGTCTGTGAC 382
Db      21  PheSerLYARGARGhrgchLYleuNENLYSILagInGInIleSerValLeuCYasp 40

QY      383  GCGGAGGTGCGCGTCATGCTCTTCTTCCCCAAAGGCAAGCTCTATAGAGTACGCCACGAC 442
Db      41  AlagILValSerIleuIleValPheSerhISysgLYleuPheGILYrSerSerGlu 60

QY      443  TTCAGCATGACAAATTTCTTAACGTTATGAGCGCTCTTATNGCTGAAAAAGCTCTT 502
Db      61  SerCYMeGILNLYValleuGILNLYrGILNLYrSerLYrAlagILNLYrGILNLeu 80

QY      503  ATTTCAGCTGAATCT-----GAAAGTGAAGGAAATTTGGTGCACGAATACAGGAACTT 556
Db      81  IleAlaPheaspSerhISerValasmlagInhIhrSerntPserMeGILYrSerArgLeu 100

QY      557  AAGCGAAGATTGAGACCATACAAAAA 583
Db      101  LysAlaLYsILlegILNLeuGILNLYrG 109

RESULT 11
US-09-853-450-14
; Sequence 14, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 14
; LENGTH: 150
; TYPE: PRF
; ORGANISM: Brassica oleracea var. botrytis
; FEATURE:
; OTHER INFORMATION: CAULIFLOWER (CAL)
US-09-853-450-14

Alignment Scores:
Pred. No.:          3.08e-29          Length:          150

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Percent Similarity: 85.98% Conservative: 17
Best Local Similarity: 70.09% Mismatches: 15
Query Match: 38.74% Indels: 0
DB: 9 Gaps: 0

US-10-020-338-8 (1-593) x US-09-978-981-087A-2 (1-242)

QY 263 ATGGGTCCGGCAGAGTGCAGTGAAGCCGATAGAAACAAGATAATTCGCGAGGTGACC 322
DB 1 MetGlyArgGlyArgValGlnLeuLysArgGlnLeuLysAlaHisLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAAAGCCCGCAGCGGCTCCGAGAAAGGCGCAGCATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgGlnSerGlyLeuLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40
QY 383 GCGGAGGTGCGCGTCATCTCTTCTCCCAAGGCAAGCCTCTATGATGACCCGAC 442
DB 41 AlaGlnValAlaLeuIleValPheSerSerLysGlyLeuLeuPheGlnLysSerThrAsp 60
QY 443 TCCAGCATGACAAATTTTGAACGTTATGACGCTACTCTTATGCTGAAGGCTCTT 502
DB 61 SerCysMetGlnArgIleLeuGlnArgGlyrAspArgGlyLeuLysSerAspLysGlnLeu 80
QY 503 ATTTGACGTGAATCTGAAAGTGAAGGAAATTGGTCCAGAAATPACAGAACTTAAGGCG 562
DB 81 ValGlyArgAspValSerGlnSerGlnAsnTrpValLeuGlnHisAlaLysLeuLysAla 100
QY 563 AAGATTGAGACCATACAAAAA 583
DB 101 ArgValGlnValLeuGlnLys 107

RESULT 7

US-09-978-382A-2
Sequence 2, Application US/0978382A
Publication No. US20020194647A1
GENERAL INFORMATION:
APPLICANT: Vanofsky, Martin F.
APPLICANT: Liljgren, Sarah
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
FILE REFERENCE: 19452A-000930US
CURRENT APPLICATION NUMBER: US/09/978,382A
PRIOR FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/090,649
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 09/339,998
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 242
TYPE: PRT
ORGANISM: Arabidopsis sp.
US-09-978-382A-2

Alignment Scores:

Pred. No.: 1,89e-30 Length: 242
Score: 399.00 Matches: 75
Percent Similarity: 85.98% Conservative: 17
Best Local Similarity: 70.09% Mismatches: 15
Query Match: 38.74% Indels: 0
DB: 9 Gaps: 0

US-10-020-338-8 (1-593) x US-09-978-382A-2 (1-242)

QY 263 ATGGGTCCGGCAGAGTGCAGTGAAGCCGATAGAAACAAGATAATTCGCGAGGTGACC 322
DB 1 MetGlyArgGlyArgValGlnLeuLysArgGlnLeuLysAlaHisLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAAAGCCCGCAGCGGCTCCGAGAAAGGCGCAGCATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgGlnSerGlyLeuLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40

QY 383 GCGGAGGTGCGCGTCATCTCTTCTCCCAAGGCAAGCCTCTATGATGACCCGAC 442
DB 41 AlaGlnValAlaLeuIleValPheSerSerLysGlyLeuLeuPheGlnLysSerThrAsp 60
QY 443 TCCAGCATGACAAATTTTGAACGTTATGACGCTACTCTTATGCTGAAGGCTCTT 502
DB 61 SerCysMetGlnArgIleLeuGlnArgGlyrAspArgGlyLeuLysSerAspLysGlnLeu 80
QY 503 ATTTGACGTGAATCTGAAAGTGAAGGAAATTGGTCCAGAAATPACAGAACTTAAGGCG 562
DB 81 ValGlyArgAspValSerGlnSerGlnAsnTrpValLeuGlnHisAlaLysLeuLysAla 100
QY 563 AAGATTGAGACCATACAAAAA 583
DB 101 ArgValGlnValLeuGlnLys 107

RESULT 8

US-09-978-740A-2
Sequence 2, Application US/09978740A
Publication No. US2003005481A1
GENERAL INFORMATION:
APPLICANT: Vanofsky, Martin F.
APPLICANT: Liljgren, Sarah
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
FILE REFERENCE: 19452A-000960US
CURRENT APPLICATION NUMBER: US/09/978,740A
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/090,649
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 09/339,998
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 242
TYPE: PRT
ORGANISM: Arabidopsis sp.
US-09-978-740A-2

Alignment Scores:

Pred. No.: 1,89e-30 Length: 242
Score: 399.00 Matches: 75
Percent Similarity: 85.98% Conservative: 17
Best Local Similarity: 70.09% Mismatches: 15
Query Match: 38.74% Indels: 0
DB: 9 Gaps: 0

US-10-020-338-8 (1-593) x US-09-978-740A-2 (1-242)

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QY 323 TTCTCCAAAGCCCGCAGCGGCTCCGAGAAAGGCGCAGCATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgGlnSerGlyLeuLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40
QY 383 GCGGAGGTGCGCGTCATCTCTTCTCCCAAGGCAAGCCTCTATGATGACCCGAC 442
DB 41 AlaGlnValAlaLeuIleValPheSerSerLysGlyLeuLeuPheGlnLysSerThrAsp 60
QY 443 TCCAGCATGACAAATTTTGAACGTTATGACGCTACTCTTATGCTGAAGGCTCTT 502
DB 61 SerCysMetGlnArgIleLeuGlnArgGlyrAspArgGlyLeuLysSerAspLysGlnLeu 80
QY 503 ATTTGACGTGAATCTGAAAGTGAAGGAAATTGGTCCAGAAATPACAGAACTTAAGGCG 562
DB 81 ValGlyArgAspValSerGlnSerGlnAsnTrpValLeuGlnHisAlaLysLeuLysAla 100
QY 563 AAGATTGAGACCATACAAAAA 583

Best Local Similarity: 99.09% Mismatches: 1
 Query Match: 54.47% Indels: 0
 DB: 9 Gaps: 0

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 DB 21 PheSerLysArgArgSerGlnLeuLysLysAlaHisGlnIleSerValLeuCyAsp 40
 QY 383 GCGAGGTGCGCGTCATGCTTCTTCCCGAAAGCGCAAGCTTATAGTACGCCACGAC 442
 DB 41 AlaGlnValAlaValIleValPheSerProLysGlyLeuLeuLysGlnIleValThrAsp 60
 QY 443 TCCAGCATGACAAATTTCTTGAAGCTTATGAGCGGCTACTTATGCTGAAAAGGCTTT 502
 DB 61 SerArgMetAspLysIleLeuGlnArgIleGlnLysSerIleValGlnLysAlaLeu 80
 QY 503 ATTCAGCTGAATCTGAAGTGAAGGGAATGTGCGCAGATACAGAACTTAAGCGC 562
 DB 81 IleSerAlaGlnSerGlnSerGlnLysGlnIleValThrPheGlnIleValArgLysLeuLysAla 100
 QY 563 AAGATTGAGACCATCAAAAATCTCAAG 592
 DB 101 LysIleGlnLysIleGlnLysCysHisLys 110

RESULT 2

US-09-853-450-4
 / Sequence 4, Application US/09853450
 / Publication No. US20020194645A1
 / GENERAL INFORMATION:
 / APPLICANT: Vanofsky, Martin F.
 / APPLICANT: Pelaz, Soraya
 / APPLICANT: Ditle, Gary
 / APPLICANT: The Regents of the University of California
 / TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
 / FILE REFERENCE: 19452A-002400US
 / CURRENT APPLICATION NUMBER: US/09/853,450
 / NUMBER OF SEQ ID NOS: 61
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 4
 / LENGTH: 253
 / TYPE: PRT
 / ORGANISM: Brassica oleracea
 / FEATURE:
 / OTHER INFORMATION: APETALAI (AP1)

US-09-853-450-4

Alignment Scores:

Pred. No.: 2,87e-33 Length: 253
 Score: 428.00 Matches: 82
 Percent Similarity: 89.72% Conservative: 14
 Best Local Similarity: 76.64% Mismatches: 11
 Query Match: 41.55% Indels: 0
 DB: 9 Gaps: 0

US-10-020-338-8 (1-593) x US-09-853-450-4 (1-253)

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 QY 323 TTCTCCAGCGCGCGAAGCGGCTCTTGAAGAGCGCGACAGATCTCCGCTCTGTGAC 382
 DB 21 PheSerLysArgArgSerGlnLeuLysLysAlaHisGlnIleSerValLeuCyAsp 40
 QY 383 GCGAGGTGCGCGTCATGCTTCTTCCCGAAAGCGCAAGCTTATAGTACGCCACGAC 442

DB 41 AlaGlnValAlaValIleValPheSerHisLysGlyLysLeuPheGlnLysSerThrAsp 60

QY 443 TCCAGCATGACAAATTTCTTGAAGCTTATGAGCGGCTACTTATGCTGAAAAGGCTTT 502

DB 61 SerCysMetGlnLysIleLeuGlnLysArgIleGlnLysSerIleValGlnLysAlaLeu 80

QY 503 ATTCAGCTGAATCTGAAGTGAAGGGAATGTGCGCAGATACAGAACTTAAGCGC 562

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QY 563 AAGATTGAGACCATCAAAA 583

DB 101 LysIleGlnLysLeuGlnLysArg 107

RESULT 3

US-09-853-450-2
 / Sequence 2, Application US/09853450
 / Publication No. US20020194645A1
 / GENERAL INFORMATION:
 / APPLICANT: Vanofsky, Martin F.
 / APPLICANT: Pelaz, Soraya
 / APPLICANT: Ditle, Gary
 / APPLICANT: The Regents of the University of California
 / TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
 / FILE REFERENCE: 19452A-002400US
 / CURRENT APPLICATION NUMBER: US/09/853,450
 / NUMBER OF SEQ ID NOS: 61
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 2
 / LENGTH: 256
 / TYPE: PRT
 / ORGANISM: Arabidopsis thaliana
 / FEATURE:
 / OTHER INFORMATION: APETALAI (AP1)

US-09-853-450-2

Alignment Scores:

Pred. No.: 7.06e-33 Length: 256
 Score: 424.00 Matches: 82
 Percent Similarity: 88.79% Conservative: 13
 Best Local Similarity: 76.64% Mismatches: 12
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 DB: 9 Gaps: 0

US-10-020-338-8 (1-593) x US-09-853-450-2 (1-256)

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 QY 323 TTCTCCAGCGCGCGAAGCGGCTCTTGAAGAGCGCGACAGATCTCCGCTCTGTGAC 382
 DB 21 PheSerLysArgArgSerGlnLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40
 QY 383 GCGAGGTGCGCGTCATGCTTCTTCCCGAAAGCGCAAGCTTATAGTACGCCACGAC 442
 DB 41 AlaGlnValAlaValIleValPheSerHisLysGlyLysLeuPheGlnLysSerThrAsp 60
 QY 443 TCCAGCATGACAAATTTCTTGAAGCTTATGAGCGGCTACTTATGCTGAAAAGGCTTT 502
 DB 61 SerCysMetGlnLysIleLeuGlnLysArgIleGlnLysSerIleValGlnLysAlaLeu 80
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 DB 81 IleAlaProGlnSerAspValAsnThrAsnThrSerMetGlnLysAsnArgLeuLysAla 100
 QY 563 AAGATTGAGACCATCAAAA 583
 DB 101 LysIleGlnLysLeuGlnLysArg 107

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 24, 2003, 14:09:43 ; Search time 28.5 Seconds
(without alignments)
4502.922 Million cell updates/sec

Title: US-10-020-338-8

Perfect score: 1030
Sequence: 1 cccggtcgaccagcgtccg.....catcaaaaatgtcacaagc 593

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Total number of hits satisfying chosen parameters: 835558

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published Applications AA:

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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2	428	41.6	253	US-09-853-450-4
3	424	41.2	256	US-09-853-450-2
4	422	41.0	255	US-09-853-450-6

5	399	38.7	242	US-09-978-729A-2	Sequence 2, Appli
6	399	38.7	242	US-09-981-087A-2	Sequence 2, Appli
7	399	38.7	242	US-09-978-382A-2	Sequence 2, Appli
8	399	38.7	242	US-09-978-740A-2	Sequence 2, Appli
9	399	38.7	242	US-09-978-730-2	Sequence 2, Appli
10	399	38.7	242	US-09-978-730-2	Sequence 2, Appli
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44	399	38.7	242	US-09-978-730-2	Sequence 2, Appli
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ALIGNMENTS

RESULT 1
US-09-853-450-8
; Sequence 8, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Vanoesky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: APETALAI (Apl)

US-09-853-450-8

Alignment Scores:
Pred. No.: 3,31e-46
Score: 561.00
Percent Similarity: 99.09%

Length: 273
Matches: 109
Conservative: 0

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APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Maize and Cauliflower APETALA1 Gene
TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,227
FILING DATE: 05-JUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2143
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-655-227-2

Alignment Scores:
Pred. No.: 1.13e-37 Length: 256
Score: 424.00 Matches: 82
Percent Similarity: 88.79% Conservative: 13
Best Local Similarity: 76.64% Mismatches: 12
Query Match: 41.17% Indels: 0
DB: 3 Gaps: 0

US-10-020-338-8 (1-593) x US-08-655-227-2 (1-256)

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DB 1 MetGlyArgGlyArgValGlnLeuLysArgIleGlnLysIleAsnArgGlnValThr 20
323 TTCTCCAAAGCGCGCAACGGCTCTGAAGAGCGCGACAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgLysGlnLeuLysValAlaHisGlnIleSerValLeuGlyAsp 40
QY 383 GCGGAGTGGCCGTCATCGTCTTCTCCCAAGCGCAAGCTCATAGTAGCGCACCGAC 442
DB 41 AlaGlnValAlaLeuValAlaPheSerHisLysGlnLeuPheGlnIleSerValLeuGlyAsp 60
QY 443 TCCAGCATGACAAATTTCTGAACGTTATGACGCTACTCTATGCTGAAGAGCTTT 502
DB 61 SerCysMetGlnLysIleLeuGlnArgTyrGlnArgTyrSerTyrAlaGlnArgGlnLeu 80
QY 503 ATTTGAGTGAATCTGAAGTGAAGGAAATTTGGTGCACGATATACAGAACTTAAGCGC 562
DB 81 IleAlaProGlnSerAspValAsnThrAsnTrpSerMetGlnLysAsnArgLeuLysAla 100
QY 563 AAGATTGACACCATCAAAA 583
DB 101 LysIleGlnLeuLeuGlnArg 107

Search completed: June 24, 2003, 14:13:23
Job time : 17.5 secs

ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/576,156
FILING DATE: 12-21-95
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,336
FILING DATE: 12-21-94
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07251/013001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-576-156-2

Alignment Scores:
Pred. No.: 1,126-37 Length: 255
Score: 424.00 Matches: 82
Percent Similarity: 88.79% Conservative: 13
Best Local Similarity: 76.64% Mismatches: 12
Query Match: 41.17% Indels: 0
DB: Gaps: 0

US-10-020-338-8 (1-593) x US-08-576-156-2 (1-255)

QY 263 ATGGGTCGGCGGAGGTGAGCGGATGAGACAGATAAATGCGCGAGTACC 322
DB 1 MetGlyArgGlyArgValGlnLeuLysArgIleGluAsnLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAGCGCGCGCAACGGCTCTGTAAGAGCGCACAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgIleGlyLeuLeuLysLysAlaHisGluIleSerValLeuCySer 40
QY 383 GCGAGGTGCGCGCTCATCGTCTTCTCCCAAGGCAAGAGCTGTATGATGACGCCACGAC 442
DB 41 AlaGluValAlaLeuValAlaPheSerHisLysGlyLysLeuPheGluLysSerThrAsp 60
QY 443 TCCAGATGAGCAAAATTTCTGAACGTTATGACGCTACTTATGCTGAAGAGCTTT 502
DB 61 SerCysMetGluLysIleLeuGluArgLysGluArgLysSerLysAlaGluArgGlnLeu 80
QY 503 ATTTCAGCTGAATCTGAAGAGTGAAGGAATTGCTGCGACGATACAGAACTTAAGCG 562
DB 81 IleAlaProGluSerAspValAsnThrAsnThrSerMetGluLysAsnArgLeuLysAla 100
QY 563 AAGATTGAGACCATCAAAAA 583
DB 101 LysIleGluLeuGluArg 107

RESULT 14
US-08-659-188-2
Sequence 2, Application US/08659188
Patent No. 6002069
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.

TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
TITLE OF INVENTION: Reproductive Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,188
FILING DATE: 05-JUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-188-2

Alignment Scores:
Pred. No.: 1,136-37 Length: 256
Score: 424.00 Matches: 82
Percent Similarity: 88.79% Conservative: 13
Best Local Similarity: 76.64% Mismatches: 12
Query Match: 41.17% Indels: 0
DB: Gaps: 0

US-10-020-338-8 (1-593) x US-08-659-188-2 (1-256)

QY 263 ATGGGTCGGCGGAGGTGAGCGGATGAGACAGATAAATGCGCGAGTACC 322
DB 1 MetGlyArgGlyArgValGlnLeuLysArgIleGluAsnLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAGCGCGCGCAACGGCTCTGTAAGAGCGCACAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgIleGlyLeuLeuLysLysAlaHisGluIleSerValLeuCySer 40
QY 383 GCGAGGTGCGCGCTCATCGTCTTCTCCCAAGGCAAGAGCTGTATGATGACGCCACGAC 442
DB 41 AlaGluValAlaLeuValAlaPheSerHisLysGlyLysLeuPheGluLysSerThrAsp 60
QY 443 TCCAGATGAGCAAAATTTCTGAACGTTATGACGCTACTTATGCTGAAGAGCTTT 502
DB 61 SerCysMetGluLysIleLeuGluArgLysGluArgLysSerLysAlaGluArgGlnLeu 80
QY 503 ATTTCAGCTGAATCTGAAGAGTGAAGGAATTGCTGCGACGATACAGAACTTAAGCG 562
DB 81 IleAlaProGluSerAspValAsnThrAsnThrSerMetGluLysAsnArgLeuLysAla 100
QY 563 AAGATTGAGACCATCAAAAA 583
DB 101 LysIleGluLeuGluArg 107

RESULT 15
US-08-655-227-2
Sequence 2, Application US/08655227
Patent No. 6025483
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/149,976
FILING DATE: 09-SEP-1998
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/592,214
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 3291
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-149-976-4

Alignment Scores:
Pred. No.: 4,14e-38 Length: 253
Score: 428.00 Matches: 82
Percent Similarity: 89.72% Conservative: 14
Best Local Similarity: 76.64% Mismatches: 11
Query Match: 41.55% Indels: 0
Gaps: 0

US-10-020-338-8 (1-593) x US-09-149-976-4 (1-253)

QY 263 ATGGGTCGGCGGCAAGTGCAGTGAAGCGGATGAGAAACAAGTAATGGCGAGTGACC 322
DB 1 MetGlyArgGlyArgValGlnLeuLysArgGlnLeuLysLeuValThr 20
QY 323 TTCTCCAAAGCGCGGCAAGCGGCTCCGGAAGAGCGGCAAGATCCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgValGlnLeuMetLysLysAlaHisGlnLysSerValLeuGlySer 40
QY 383 GCGAGGTGCGCGCTCATGCTCTTCTCCCAAGGCAAGCTCATGAGTACGCCACCGAC 442
DB 41 AlaGlnValAlaLeuValValPheSerHisLysGlyLysLeuPheGlnLysSerThrAsp 60
QY 443 TCACAGATGACAAATTTCTTGAAGCTTATGAGCGCTACTCTTATGCTGAAAAGCTCTT 502
DB 61 SerCysMetGlnLysLysLeuGlnArgTyrGlnArgTyrSerTyrAlaGlnArgGlnLeu 80
QY 503 ATTTGAGCTGAATCTGAAGTGAAGGAATTTGTCGACGAAATACAGAACTTAAGGCG 562
DB 81 IleAlaProGlnSerAspSerAsnThrAsnTrpSerMetCysLysArgLeuLysAla 100
QY 563 AAGATTGAGACCATACAAA 583
DB 101 LysIleGlnLeuLeuGlnArg 107

RESULT 12
US-09-398-326-4
Sequence 4, Application US/09398326
Patent No. 6355863
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
TITLE OF INVENTION: Reproductive Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California

COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/198,326
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/659,188
FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 3739
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-398-326-4

Alignment Scores:
Pred. No.: 4,14e-38 Length: 253
Score: 428.00 Matches: 82
Percent Similarity: 89.72% Conservative: 14
Best Local Similarity: 76.64% Mismatches: 11
Query Match: 41.55% Indels: 0
Gaps: 0

US-10-020-338-8 (1-593) x US-09-398-326-4 (1-253)

QY 263 ATGGGTCGGCGGCAAGTGCAGTGAAGCGGATGAGAAACAAGTAATGGCGAGTGACC 322
DB 1 MetGlyArgGlyArgValGlnLeuLysArgGlnLeuLysLeuValThr 20
QY 323 TTCTCCAAAGCGCGGCAAGCGGCTCCGGAAGAGCGGCAAGATCCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgValGlnLeuMetLysLysAlaHisGlnLysSerValLeuGlySer 40
QY 383 GCGAGGTGCGCGCTCATGCTCTTCTCCCAAGGCAAGCTCATGAGTACGCCACCGAC 442
DB 41 AlaGlnValAlaLeuValValPheSerHisLysGlyLysLeuPheGlnLysSerThrAsp 60
QY 443 TCACAGATGACAAATTTCTTGAAGCTTATGAGCGCTACTCTTATGCTGAAAAGCTCTT 502
DB 61 SerCysMetGlnLysLysLeuGlnArgTyrGlnArgTyrSerTyrAlaGlnArgGlnLeu 80
QY 503 ATTTGAGCTGAATCTGAAGTGAAGGAATTTGTCGACGAAATACAGAACTTAAGGCG 562
DB 81 IleAlaProGlnSerAspSerAsnThrAsnTrpSerMetCysLysArgLeuLysAla 100
QY 563 AAGATTGAGACCATACAAA 583
DB 101 LysIleGlnLeuLeuGlnArg 107

RESULT 13
US-08-576-156-2
Sequence 2, Application US/08576156
Patent No. 5844119
GENERAL INFORMATION:
APPLICANT: Weigel, Detlef
TITLE OF INVENTION: Genetically Modified Plants Having Modulated
TITLE OF INVENTION: Flower Development
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/655,227
 FILING DATE: 05-JUN-1996
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-UD 2143
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-655-227-4

Alignment Scores:
 Seq. No.: 4,146-38 Length: 253
 Score: 428.00 Matches: 82
 Percent Similarity: 89.72% Conservative: 14
 Best Local Similarity: 76.64% Mismatches: 11
 Query Match: 41.55% Indels: 0
 DB: 3 Gaps: 0

US-10-020-338-8 (1-593) x US-08-655-227-4 (1-253)

QY 263 ATGGGTCCGGGCGGAGGTGAGTGAAGCGGATGAGAGCAAGATTAATCGGAGGTGACC 322
 DB 1 MetGlyArgGlyArgValGlnLeuYsArgGlnLeuYsIleAsnArgGlnValThr 20
 QY 323 TTCTCCAGCGCGGCGGAGCGGCTCTGAAAGAGCGGCGAGATCTCCGCTCTGTGAC 382
 DB 21 PheSerLysArgValGlnLeuMetLysValIleGlnLeuSerValLeuYsAsp 40
 QY 383 GGGAGGTGCGGCGGCTCTGCTTCCCGCAAGGAGGCTGATAGTATGAGCGGACCGAC 442
 DB 41 AlaGlnValAlaLeuValIlePheSerHisLysGlyLysLeuPheGlnLeuSerThrAsp 60
 QY 443 TCCAGCATGACAAATCTTGAACGTATGAGCGGCTCTTATGCTGAAAGGCTCTT 502
 DB 61 SerCysMetGlnLysIleLeuGlnArgTyrGlnArgTyrSerThrIleGlnArgGlnLeu 80
 QY 503 ATTTCAGCTGAATCTGAAAGTGAGGAAATGTCGCCAGATACAGGAACTTAAGCGC 562
 DB 81 IleAlaProGlnSerAspSerIleThrAsnTrpSerMetGlnLysAsnArgLeuYsAla 100
 QY 563 AAGATTGAGACCATACAAAA 583
 DB 101 LysIleGlnLeuGlnArg 107

RESULT 10
 US-08-655-241-4
 ; Sequence 4, Application US/08655241
 ; Patent No. 6025543
 ; GENERAL INFORMATION:
 ; APPLICANT: Yanofsky, Martin F.
 ; APPLICANT: Weigel, Declaf
 ; TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
 ; TITLE OF INVENTION: Development and Methods of Making Same
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell and Flores
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/655,241
 FILING DATE: 05-JUN-1996
 CLASSIFICATION: CLASS 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-UD 1894
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-655-241-4

Alignment Scores:
 Seq. No.: 4,146-38 Length: 253
 Score: 428.00 Matches: 82
 Percent Similarity: 89.72% Conservative: 14
 Best Local Similarity: 76.64% Mismatches: 11
 Query Match: 41.55% Indels: 0
 DB: 3 Gaps: 0

US-10-020-338-8 (1-593) x US-08-655-241-4 (1-253)

QY 263 ATGGGTCCGGGCGGAGGTGAGTGAAGCGGATGAGAGCAAGATTAATCGGAGGTGACC 322
 DB 1 MetGlyArgGlyArgValGlnLeuYsArgGlnLeuYsIleAsnArgGlnValThr 20
 QY 323 TTCTCCAGCGCGGCGGAGCGGCTCTGAAAGAGCGGCGAGATCTCCGCTCTGTGAC 382
 DB 21 PheSerLysArgValGlnLeuMetLysValIleGlnLeuSerValLeuYsAsp 40
 QY 383 GGGAGGTGCGGCGGCTCTGCTTCCCGCAAGGAGGCTGATAGTATGAGCGGACCGAC 442
 DB 41 AlaGlnValAlaLeuValIlePheSerHisLysGlyLysLeuPheGlnLeuSerThrAsp 60
 QY 443 TCCAGCATGACAAATCTTGAACGTATGAGCGGCTCTTATGCTGAAAGGCTCTT 502
 DB 61 SerCysMetGlnLysIleLeuGlnArgTyrGlnArgTyrSerThrIleGlnArgGlnLeu 80
 QY 503 ATTTCAGCTGAATCTGAAAGTGAGGAAATGTCGCCAGATACAGGAACTTAAGCGC 562
 DB 81 IleAlaProGlnSerAspSerIleThrAsnTrpSerMetGlnLysAsnArgLeuYsAla 100
 QY 563 AAGATTGAGACCATACAAAA 583
 DB 101 LysIleGlnLeuGlnArg 107

RESULT 11
 US-09-149-976-4
 ; Sequence 4, Application US/09149976
 ; Patent No. 6127123
 ; GENERAL INFORMATION:
 ; APPLICANT: Yanofsky, Martin F.
 ; APPLICANT: Weigel, Declaf
 ; TITLE OF INVENTION: Cauliflower Floral Meristem Identity
 ; TITLE OF INVENTION: Genes and Methods of Using Same
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

FILED DATE: 26-JAN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1927
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-592-214A-4

Alignment Scores:
Pred. No.: 4,146-38 Length: 253
Score: 428.00 Matches: 82
Percent Similarity: 89.72% Conservative: 14
Best Local Similarity: 76.64% Mismatches: 11
Query Match: 41.55% Indels: 0
DB: 2 Gaps: 0

US-10-020-338-8 (1-593) x US-08-592-214A-4 (1-253)

QY 263 ATGGGTCGGCGGCGGAGCTGAAGCGGATAGAGCAAGATAATCGCGAGTGACC 322
DB 1 MetGLYArgGLYArgValGlnLeuLysArgIleGlnLysLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAGCGCGCGCAACGGGCTCTGAAGAGCGCAGAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgIleGlnLeuMetLysLysAlaHisGlnIleSerValLeuGlySer 40
QY 383 GCGAGGTGGCGCTCATCGTCTTCTCCCAAGGCAAGCTATAGTAGCGCCACCGAC 442
DB 41 AlaGlnValAlaLeuValAlaPheSerHisLysGlyLysLeuPheGlnLysSerThrAsp 60
QY 443 TCCAGCATGAGCAAAATTTCTGAAGCTTATGAGCGCTACTGCTATAGCTGAAGAGCTTT 502
DB 61 SerCysMetGlnLysLysIleLeuGlnArgTyrGlnArgTyrSerTyrAlaGlnArgGlnLeu 80
QY 503 ATTTCAGTGAATCTGAAGTAGAGGAAATTTGGTGCACGAAATACAGAACTTAAGGCG 562
DB 81 IleAlaProGlnSerAspSerAsnThrAsnThrSerMetGlnLysTrpAsnArgLeuLysAla 100
QY 563 AAGATTGAGACCATACAAAA 583
DB 101 LysIleGlnLeuGlnArg 107

RESULT 8

US-08-659-188-4
Sequence 4, Application US/08659188
Patent No. 6002069
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
TITLE OF INVENTION: Reproductive Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/659,188
FILED DATE: 05-JUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-188-4

Alignment Scores:
Pred. No.: 4,146-38 Length: 253
Score: 428.00 Matches: 82
Percent Similarity: 89.72% Conservative: 14
Best Local Similarity: 76.64% Mismatches: 11
Query Match: 41.55% Indels: 0
DB: 3 Gaps: 0

US-10-020-338-8 (1-593) x US-08-659-188-4 (1-253)

QY 263 ATGGGTCGGCGGCGGAGCTGAAGCGGATAGAGCAAGATAATCGCGAGTGACC 322
DB 1 MetGLYArgGLYArgValGlnLeuLysArgIleGlnLysLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAGCGCGCGCAACGGGCTCTGAAGAGCGCAGAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgIleGlnLeuMetLysLysAlaHisGlnIleSerValLeuGlySer 40
QY 383 GCGAGGTGGCGCTCATCGTCTTCTCCCAAGGCAAGCTATAGTAGCGCCACCGAC 442
DB 41 AlaGlnValAlaLeuValAlaPheSerHisLysGlyLysLeuPheGlnLysSerThrAsp 60
QY 443 TCCAGCATGAGCAAAATTTCTGAAGCTTATGAGCGCTACTGCTATAGCTGAAGAGCTTT 502
DB 61 SerCysMetGlnLysLysIleLeuGlnArgTyrGlnArgTyrSerTyrAlaGlnArgGlnLeu 80
QY 503 ATTTCAGTGAATCTGAAGTAGAGGAAATTTGGTGCACGAAATACAGAACTTAAGGCG 562
DB 81 IleAlaProGlnSerAspSerAsnThrAsnThrSerMetGlnLysTrpAsnArgLeuLysAla 100
QY 563 AAGATTGAGACCATACAAAA 583
DB 101 LysIleGlnLeuGlnArg 107

RESULT 9

US-08-655-227-4
Sequence 4, Application US/08655227
Patent No. 6025483
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Maize and Cauliflower APTERAL Gene
TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

REFERENCE/DOCKET NUMBER: P-UD 3291

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 273 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-149-976-8

Alignment Scores:

Pred. No.:	1,736-52	Length:	273
Score:	561.00	Matches:	109
Percent Similarity:	99.09%	Conservative:	0
Best Local Similarity:	99.09%	Mismatches:	1
Query Match:	54.47%	Indels:	0
DB:	3	Gaps:	0

US-10-020-338-8 (1-593) x US-09-149-976-8 (1-273)

QY 263 ATGGTCGCGGCAAGGTGACGTGAAGCGGATAGAGAACAGATAATCGGAGGTGACC 322

DB 1 MetGlyArgGlyLysValGlnLeuYsArgIleGluAsnLysIleAsnArgGlnValThr 20

QY 323 TTCTCCAGCGCGGCAAGCGGCTCTGAAAGAGCGGCAAGATCTCCGCTCTGTGAC 382

DB 21 PheSerLysArgLysAsnGlyLeuLeuLysLysAlaHisGlnIleSerValLeuGlyAsp 40

QY 383 GGGAGGTCGCGGTCATCTCTCTCCCAAGGCAAGCTCATATGATAGCCACCGAC 442

DB 41 AlaGlnValAlaValIleValPheSerProLysGlyLysLeuYrLValThrAsp 60

QY 443 TCCAGCATGACCAAAATTTCTTGAACGTTATGACCGCTACTTATGCTGAAAAGCTCTT 502

DB 61 SerArgMetAspLysIleLeuGlnArgTyrGlnArgTyrSerTyrAlaGlnLysAlaLeu 80

QY 503 ATTTCAGCTGAATCTGAAAGTGAAGGAAATTTGTCGCAAGATACGAACTTAAGGCG 562

DB 81 IleSerAlaGlnSerGlnSerGlnLysArgTyrPheGlnLysArgLysLeuYsAla 100

QY 563 AGATTGAGACCATACAAAAATGTCAAG 592

DB 101 LysIleGlnThrIleGlnLysCysHisLys 110

RESULT 6

US-09-398-326-8

Sequence 8, Application US/09398326

Patent No. 6355863

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.

TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early

TITLE OF INVENTION: Reproductive Development and Methods of Making Same

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/659,188

FILING DATE: 05-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 3739

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 273 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-398-326-8

Alignment Scores:

Pred. No.:	1,736-52	Length:	273
Score:	561.00	Matches:	109
Percent Similarity:	99.09%	Conservative:	0
Best Local Similarity:	99.09%	Mismatches:	1
Query Match:	54.47%	Indels:	0
DB:	4	Gaps:	0

US-10-020-338-8 (1-593) x US-09-398-326-8 (1-273)

QY 263 ATGGTCGCGGCAAGGTGACGTGAAGCGGATAGAGAACAGATAATCGGAGGTGACC 322

DB 1 MetGlyArgGlyLysValGlnLeuYsArgIleGluAsnLysIleAsnArgGlnValThr 20

QY 323 TTCTCCAGCGCGGCAAGCGGCTCTGAAAGAGCGGCAAGATCTCCGCTCTGTGAC 382

DB 21 PheSerLysArgLysAsnGlyLeuLeuLysLysAlaHisGlnIleSerValLeuGlyAsp 40

QY 383 GGGAGGTCGCGGTCATCTCTCTCCCAAGGCAAGCTCATATGATAGCCACCGAC 442

DB 41 AlaGlnValAlaValIleValPheSerProLysGlyLysLeuYrLValThrAsp 60

QY 443 TCCAGCATGACCAAAATTTCTTGAACGTTATGACCGCTACTTATGCTGAAAAGCTCTT 502

DB 61 SerArgMetAspLysIleLeuGlnArgTyrGlnArgTyrSerTyrAlaGlnLysAlaLeu 80

QY 503 ATTTCAGCTGAATCTGAAAGTGAAGGAAATTTGTCGCAAGATACGAACTTAAGGCG 562

DB 81 IleSerAlaGlnSerGlnSerGlnLysArgTyrPheGlnLysArgLysLeuYsAla 100

QY 563 AGATTGAGACCATACAAAAATGTCAAG 592

DB 101 LysIleGlnThrIleGlnLysCysHisLys 110

RESULT 7

US-08-592-214A-4

Sequence 4, Application US/08592214A

Patent No. 5811536

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.

TITLE OF INVENTION: Cauliflower Floral Meristem Identify

TITLE OF INVENTION: Genes and Methods of Using Same

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/592,214A

LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-655-227-8

Alignment Scores:
Pred. No.: 1.73e-52 Length: 273
Score: 561.00 Matches: 109
Percent Similarity: 99.09% Conservative: 0
Best Local Similarity: 99.09% Mismatches: 1
Query Match: 54.47% Indels: 0
Gaps: 0

US-10-020-338-8 (1-593) x US-08-655-227-8 (1-273)

QY 263 ATGGGTCGGGCGGAGGTGAGCGGATGAGACAAAGTAATCGGCGAGTGACC 322
DB 1 MetGlyArgGlyLysValGlnLeuLysArgIleGlnAsnLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAAAGCGCGCAAGCGGCTCCTGAAGAGCGCGACAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgAsnGlnLeuLysLysValahisGlnIleSerValLeuLysAsp 40
QY 383 GCGAGGTGCGCGTCATGCTCTTCTCCCAAGGCAAGCTTATGAGTACGCCACGAC 442
DB 41 AlaGlnValAlaValIleValPheSerProLysGlyLysLeuLysArgIleValThrAsp 60
QY 443 TCCAGCATGACAAATTTCTTGAACGTTATGAGCGCTACTTATGCTGAAGAGGCTCTT 502
DB 61 SerArgMetAspLysIleLeuGlnArgIleGlnLysArgIleValThrAsp 80
QY 503 ATTGAGCTGAATCTGAAGTGAAGGGAATGTCGCCAAGTATACAGAACTTAAGGCG 562
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QY 563 AAGATTGAGACCATACAAATGTCCACAG 592
DB 101 LysIleGlnThrIleGlnLysCysHisLys 110

RESULT 4
US-08-655-241-8
Sequence 8, Application US/08655241
Patent No. 6025543
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
TITLE OF INVENTION: Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,241
FILING DATE: 05-JUN-1996
CLASSIFICATION: CLASS 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1894
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-655-241-8

Alignment Scores:
Pred. No.: 1.73e-52 Length: 273
Score: 561.00 Matches: 109
Percent Similarity: 99.09% Conservative: 0
Best Local Similarity: 99.09% Mismatches: 1
Query Match: 54.47% Indels: 0
Gaps: 0

US-10-020-338-8 (1-593) x US-08-655-241-8 (1-273)

QY 263 ATGGGTCGGGCGGAGGTGAGCGGATGAGACAAAGTAATCGGCGAGTGACC 322
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QY 323 TTCTCCAAAGCGCGCAAGCGGCTCCTGAAGAGCGCGACAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgAsnGlnLeuLysLysValahisGlnIleSerValLeuLysAsp 40
QY 383 GCGAGGTGCGCGTCATGCTCTTCTCCCAAGGCAAGCTTATGAGTACGCCACGAC 442
DB 41 AlaGlnValAlaValIleValPheSerProLysGlyLysLeuLysArgIleValThrAsp 60
QY 443 TCCAGCATGACAAATTTCTTGAACGTTATGAGCGCTACTTATGCTGAAGAGGCTCTT 502
DB 61 SerArgMetAspLysIleLeuGlnArgIleGlnLysArgIleValThrAsp 80
QY 503 ATTGAGCTGAATCTGAAGTGAAGGGAATGTCGCCAAGTATACAGAACTTAAGGCG 562
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QY 563 AAGATTGAGACCATACAAATGTCCACAG 592
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RESULT 5
US-09-149-976-8
Sequence 8, Application US/09149976
Patent No. 6127123
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identity
TITLE OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/149,976
FILING DATE: 09-SEP-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,214
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 24, 2003, 14:08:24 ; Search time 13.5 Seconds
(without alignments)
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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Total number of hits satisfying chosen parameters: 525148

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	561	54.5	273	3	US-08-655-241-8
5	561	54.5	273	3	US-09-149-976-8
6	561	54.5	273	4	US-09-398-326-8
7	428	41.6	253	2	US-08-592-214A-4
8	428	41.6	253	3	US-08-659-188-4
9	428	41.6	253	3	US-08-655-227-4
10	428	41.6	253	3	US-08-655-241-4
11	428	41.6	253	3	US-09-149-976-4
12	428	41.6	253	4	US-09-398-326-4

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15	424	41.2	256	3	US-08-655-227-2	Sequence 2, Appl 1
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17	424	41.2	256	4	US-09-398-326-2	Sequence 2, Appl 1
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39	386	37.5	150	3	US-09-149-976-14	Sequence 14, Appl 1
40	386	37.5	150	4	US-09-398-326-14	Sequence 14, Appl 1
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43	382	37.1	251	3	US-08-655-227-12	Sequence 12, Appl 1
44	382	37.1	251	3	US-08-655-241-12	Sequence 12, Appl 1
45	382	37.1	251	3	US-09-149-976-12	Sequence 12, Appl 1

ALIGNMENTS

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Sequence 8, Application US/08592214A
Patent No. 5811536
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identify
TITLE OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,214A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1927
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid

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PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
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PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
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PR 12-OCT-1999; 99US-0158369.
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PR 18-OCT-1999; 99US-0159584.
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PR 22-OCT-1999; 99US-0160980.
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PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
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PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
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XX
AC AAW23812;
XX
DT 11-MAY-1998 (first entry)
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DE Brassica oleracea floral meristem identity gene API product.
XX
KW Floral meristem identity gene; APETALA1; API gene;
XX flower development; transgenic plant; angiosperm.
XX
OS Brassica oleracea.
XX
PN WO9727287-A1.
XX
PD 31-JUL-1997.
XX
PF 26-JAN-1996; 96WO-US01041.
XX
PR 26-JAN-1996; 96WO-US01041.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Yanofsky MF;
XX
DR MPI; 1997-393675/36.
XX
DR N-PSDB; AAT76886 and AAT76893.
XX
PT Cauliflower floral meristem identity genes and related proteins -
XX used to develop products for converting shoot meristem to floral
XX meristem and promoting early flowering in an angiosperm
XX
PS Disclosure: Fig 2A-B; 132pp; English.
XX
XX
XX This sequence comprises the Brassica oleracea APETALA (API) gene
XX product that is involved in the conversion of shoot meristem to
XX floral meristem. B. oleracea API cDNA and genomic DNA sequences
XX are provided (see AAT76886 and AAT76893). Mutation of the API gene
XX results in replacement of a few basal flowers by inflorescence
XX shoots that are not subtended by flowers. When API is ecotopically
XX expressed in shoot meristem, the shoot meristem is converted to
XX floral meristem and early flowering can occur. The invention
XX relates to floral meristem identity genes API, LFY and especially
XX CAL (see AAT76885-97 and AAT99437) and their gene products (see
XX AAW23811-18), and their use in converting shoot meristem to floral
XX meristem and in promoting early flowering in transgenic plants,
XX especially angiosperms such as cereal plants, leguminous plants,
XX oilseed plants, trees, fruit-bearing plants or ornamental flowers.
XX
XX Sequence 253 AA;

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KM Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence; corn.

OS Zea mays subsp. mays.

XX EPI033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

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PR 04-MAY-1999; 99US-0132484.

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PR 24-MAY-1999; 99US-0135629.

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PR 18-JUN-1999; 99US-0139750.

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PR 21-JUN-1999; 99US-0139817.

PR 22-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140353.

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PR 30-JUN-1999; 99US-0141287.

PR 01-JUL-1999; 99US-0141842.

PR 01-JUL-1999; 99US-0142154.

PR 02-JUL-1999; 99US-0142055.

PR 06-JUL-1999; 99US-0142390.

PR 08-JUL-1999; 99US-0142803.

PR 09-JUL-1999; 99US-0142920.

PR 12-JUL-1999; 99US-0142977.

PR 13-JUL-1999; 99US-0143542.

PR 14-JUL-1999; 99US-0143624.

PR 15-JUL-1999; 99US-0144005.

PR 16-JUL-1999; 99US-0144085.

PR 19-JUL-1999; 99US-0144086.

PR 19-JUL-1999; 99US-0144331.

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PR 19-JUL-1999; 99US-0144333.

PR 19-JUL-1999; 99US-0144334.

PR 19-JUL-1999; 99US-0144335.

PR 20-JUL-1999; 99US-0144352.

PR 20-JUL-1999; 99US-0144362.

PR 21-JUL-1999; 99US-0144884.

PR 21-JUL-1999; 99US-0144814.

PR 21-JUL-1999; 99US-0145086.

PR 22-JUL-1999; 99US-0145088.

PR 22-JUL-1999; 99US-0145085.

PR 22-JUL-1999; 99US-0145087.

PR 22-JUL-1999; 99US-0145089.

PR 22-JUL-1999; 99US-0145192.

PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145218.

PR 23-JUL-1999; 99US-0145224.

PR 26-JUL-1999; 99US-0145276.

PR 27-JUL-1999; 99US-0145913.

PR 27-JUL-1999; 99US-0145918.

PR 27-JUL-1999; 99US-0145919.

PR 28-JUL-1999; 99US-0145951.

PR 02-AUG-1999; 99US-0146386.

PR 02-AUG-1999; 99US-0146388.

PR 02-AUG-1999; 99US-0146389.

PR 03-AUG-1999; 99US-0147038.

PR 04-AUG-1999; 99US-0147204.

PR 05-AUG-1999; 99US-0147302.

PR 05-AUG-1999; 99US-0147192.

PR 05-AUG-1999; 99US-0147260.

PR 06-AUG-1999; 99US-0147303.

PR 06-AUG-1999; 99US-0147416.

PR 09-AUG-1999; 99US-0147493.

PR 09-AUG-1999; 99US-0147935.

PR 10-AUG-1999; 99US-0148171.

PR 11-AUG-1999; 99US-0148319.

PR 12-AUG-1999; 99US-0148341.

PR 13-AUG-1999; 99US-0148565.

PR 13-AUG-1999; 99US-0148684.

PR 16-AUG-1999; 99US-0149368.

PR 17-AUG-1999; 99US-0149175.

PR 18-AUG-1999; 99US-0149426.

PR 20-AUG-1999; 99US-0149722.

PR 20-AUG-1999; 99US-0149723.

PR 20-AUG-1999; 99US-0149929.

PR 23-AUG-1999; 99US-0149902.

PR 23-AUG-1999; 99US-0149930.

PR 25-AUG-1999; 99US-0150566.

PR 26-AUG-1999; 99US-0150884.

PR 27-AUG-1999; 99US-0151065.

PR 27-AUG-1999; 99US-0151066.

PR 27-AUG-1999; 99US-0151080.

PR 30-AUG-1999; 99US-0151303.

PR 31-AUG-1999; 99US-0151438.

PR	18-OCT-1999	990US-01553584
PR	21-OCT-1999	990US-01607041
PR	21-OCT-1999	990US-01607667
PR	21-OCT-1999	990US-01607668
PR	21-OCT-1999	990US-01607676
PR	21-OCT-1999	990US-01607700
PR	21-OCT-1999	990US-01608144
PR	21-OCT-1999	990US-01608015
PR	22-OCT-1999	990US-01608085
PR	22-OCT-1999	990US-01609881
PR	22-OCT-1999	990US-01609880
PR	22-OCT-1999	990US-01609894
PR	25-OCT-1999	990US-01614004
PR	25-OCT-1999	990US-01614005
PR	25-OCT-1999	990US-01614006
PR	25-OCT-1999	990US-01613359
PR	26-OCT-1999	990US-01613360
PR	26-OCT-1999	990US-01613621
PR	26-OCT-1999	990US-01613610
PR	28-OCT-1999	990US-01619992
PR	28-OCT-1999	990US-01619993
PR	29-OCT-1999	990US-01621412

Alignment Scores:	
Pred. No.:	5,46e-50
Score:	554.00
Percent Similarity:	99.09%
Best Local Similarity:	97.27%
Query Match:	53.79%
DB:	21
Length:	142
Matches:	107
Conservative:	2
Mismatches:	1
Indels:	0
Gaps:	0

US-10-020-338-8 (1-593) x AAG33291 (1-142)

Oy 263 ATGGGTCGGCGCAAGGTGAGCTGAAAGCCGATGTGACAAACAAGTTAATCGGCAGGTGACC 3822
 Db 1 MetGlyAArgGlyLysValGlnLeuLysAspGlieLeuAsnLysIleAsnArgGlnValThr 20
 Oy 323 TTCTCTCAAGCGCGCGCAACGGGCTCCCTGAAGAAGAGCCGACAGAGATCTCCGCTCTGTGAC 3823
 Db 21 PheSerLysArgArgAsnIleLeuLeuLysLysAlaHisGlnIleSerValLeuCybAsp 40
 Oy 383 GCGGAGGTGCGCGTCATCGTCTTCTCCGCCAAAGGCAAGCTCTATGAGTACGCCACCGAC 4422
 Db 41 AlaGlnValAlaValIleValPheSerProLysGlyLysLeuArgIuTyralaSerAsp 60
 Oy 443 TTCACAGATGACCAAAATTTCTTGACGTTATGAGCGCTACTCTTATGCTGAAAAGGCTTT 5022
 Db 61 SerArgMetAspLysIleLeuGlnArgTyGluArgLysSerTyralaGlnLysAlaLeu 80
 Oy 503 ATTTGAGCTGATCTGAAGTGAAGGGAATGGTGACAGAAATACGGAACCTTAAGCG 5622
 Db 81 IleSerIleArgLysSerGlnSerGluGlnLysArgIuTybIleGlnTyArgLysLeuLysAla 1000
 Oy 563 AAGATTGAGACCATCAAAAATGTCAACAG 592
 Db 101 LysIleGlnThrIleGlnArgCysHisLys 110

RESULT 12

ID AAB68357 standard; Protein; 270 AA.

AC	AAB68357;
XX	
DT	09-JUL-2001 (first entry)

DE Amino acid sequence of a maize ZmMAD3 protein

KW MAD3; flower development; flower structure; seed development
 KW fruit development; transgenic plant.
 KW

OS Zea mays

PN WO200131017-A2.

PD 03-MAY-2001.

XX 25-OCT-2000; 2000WO-EP10484

PR 25-OCT-1999; 99EP-0120842.

PA (SUED-) SÜDWESTDEUTSCHE SAATZUCHT
XX

PI Dresselhaus T, Heuer S, Loertz H,
XX

DR WPL; 2001-316335/33-
N-PSDB: AAF85192.

PT New polynucleotide

PT New polynucleotide encoding ZmMADS3 protein, for use in cloning and
PT expression in plant a nucleic acid sequence encoding protein
PT influencing flower structure, function and/or its seed and/or fruit
PT development

CC The present sequence represents a maize MADS protein, designated ZmMADS3
CC The ZmMADS3 protein is essential for flower development and is active
CC in flowers, in particular, in immature flowers and female flowers,
CC but also in the mature embryo sac of maize. The ZmMADS3 protein is also
CC active in nodes and adjacent cell layers. ZmMADS3 polynucleotides and
CC polypeptides are useful in transgenic flower structure, function and
CC seed or fruit development in transgenic plants.

SQ Sequence 270 AA.

Alignment scores:	
Pred. No.:	6,73e-50
Score:	554.00
Percent Similarity:	99.09%
Best Local Similarity:	97.27%
Query Match:	53.79%
DB:	22
Length:	270
Matches:	107
Conservative:	2
Mismatches:	1
Indels:	0
Gaps:	0

US-10-020-338-8 (1-593) X AAB68357 (1-270)

QY	26	ATGAGTGC	CGGCAAGGTG	CAGTGTGA	AGCAATAG	GAACAA	GATTAATTC	GGCAGGTG	CACC	322											
Db	1	Me	CGlYAr	gIyStAl	gInleu	nyAr	gIle	uInen	ySIlle	hAnAr	gInVal	Thr	20								
QY	323	TTCTCC	AAAGCCG	CGCAAG	GGGCTCT	CTGA	AGAA	GGCG	CGACG	AGATCT	CCGCTCT	TGTG	AC	382							
Db	21	Ph	Se	rIyAr	gIyAr	gIn	gInleu	nySly	SA	ah	gInle	Se	rVal	Leu	Cys	Asp	40				
QY	383	GCGAGG	TGC	CGCGT	CTCAT	CGCTT	CTTCC	CCCC	AAAG	CGCAAG	CGCTTA	TGAGT	AGCG	CCAC	CGAC	442					
Db	41	Al	gInVal	Al	Al	Al	Al	Val	Ph	Se	rPro	lyS	gIy	leu	ny	gIn	Val	Ala	Se	rAsp	60
QY	443	TC	CAGC	ATG	CAAA	AAATTT	TTGA	AGTT	ATG	AGCG	CTACT	CTTAT	GCTG	AAAA	AGCT	CTT	502				
Db	61	Se	rAr	gMe	Ar	SA	pIy	Sly	Ille	uIn	ny	gIy	gIn	Val	gIy	Se	rVal	Ala	Leu	80	
QY	503	ATTTC	AGCTGA	ATCTTA	AGATG	AGAG	GGAA	ATTG	TGTC	CCAC	GAATC	ACAG	AAAT	CTTA	AGCG	562					
Db	81	Il	Se	rAl	gIn	Se	rI	uIn	gIn	leu	ny	SA	en	rP	Cys	hI	gI	u	Val	Ala	100
QY	563	AA	GATT	GAG	CCCTA	TAA	AAAA	ATG	TAC	AC	AG	592									
Db	101	Lys	l	Se	rI	gIn	Val	Thr	l	gIn	leu	ny	Cys	hI	Sly	110					

RESULT 13

ID	AA
AAG34120	standard; Protein; 307 AA

AC AAG34120;
yy

DT	18-OCT-2000	(first entry)
YY		

DE Zea mays protein fragment SEQ ID NO: 41468.
XX

PR 28-APR-1999; 99US-0131449.
 PR 30-APR-1999; 99US-0132048.
 PR 30-APR-1999; 99US-0132407.
 PR 04-MAY-1999; 99US-0132484.
 PR 05-MAY-1999; 99US-0132485.
 PR 06-MAY-1999; 99US-0132486.
 PR 06-MAY-1999; 99US-0132487.
 PR 07-MAY-1999; 99US-0132863.
 PR 11-MAY-1999; 99US-0134256.
 PR 14-MAY-1999; 99US-0134218.
 PR 14-MAY-1999; 99US-0134219.
 PR 14-MAY-1999; 99US-0134221.
 PR 14-MAY-1999; 99US-0134370.
 PR 18-MAY-1999; 99US-0134768.
 PR 19-MAY-1999; 99US-0134941.
 PR 20-MAY-1999; 99US-0135124.
 PR 21-MAY-1999; 99US-0135353.
 PR 24-MAY-1999; 99US-0135629.
 PR 25-MAY-1999; 99US-0136021.
 PR 27-MAY-1999; 99US-0136392.
 PR 28-MAY-1999; 99US-0136782.
 PR 01-JUN-1999; 99US-0137222.
 PR 03-JUN-1999; 99US-0137528.
 PR 04-JUN-1999; 99US-0137502.
 PR 07-JUN-1999; 99US-0137724.
 PR 08-JUN-1999; 99US-0138094.
 PR 10-JUN-1999; 99US-0138540.
 PR 14-JUN-1999; 99US-0138847.
 PR 16-JUN-1999; 99US-0139119.
 PR 16-JUN-1999; 99US-0139452.
 PR 16-JUN-1999; 99US-0139453.
 PR 17-JUN-1999; 99US-0139492.
 PR 18-JUN-1999; 99US-0139454.
 PR 18-JUN-1999; 99US-0139455.
 PR 18-JUN-1999; 99US-0139456.
 PR 18-JUN-1999; 99US-0139457.
 PR 18-JUN-1999; 99US-0139458.
 PR 18-JUN-1999; 99US-0139459.
 PR 18-JUN-1999; 99US-0139460.
 PR 18-JUN-1999; 99US-0139461.
 PR 18-JUN-1999; 99US-0139462.
 PR 18-JUN-1999; 99US-0139463.
 PR 18-JUN-1999; 99US-0139750.
 PR 18-JUN-1999; 99US-0139763.
 PR 21-JUN-1999; 99US-0139817.
 PR 22-JUN-1999; 99US-0139899.
 PR 23-JUN-1999; 99US-0140353.
 PR 23-JUN-1999; 99US-0140354.
 PR 24-JUN-1999; 99US-0140695.
 PR 28-JUN-1999; 99US-0140823.
 PR 29-JUN-1999; 99US-0140991.
 PR 30-JUN-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141842.
 PR 01-JUL-1999; 99US-0142154.
 PR 02-JUL-1999; 99US-0142055.
 PR 06-JUL-1999; 99US-0142390.
 PR 08-JUL-1999; 99US-0142803.
 PR 09-JUL-1999; 99US-0142920.
 PR 12-JUL-1999; 99US-0142877.
 PR 13-JUL-1999; 99US-0143442.
 PR 14-JUL-1999; 99US-0143624.
 PR 15-JUL-1999; 99US-0144005.
 PR 16-JUL-1999; 99US-0144085.
 PR 16-JUL-1999; 99US-0144086.
 PR 19-JUL-1999; 99US-0144325.
 PR 19-JUL-1999; 99US-0144331.
 PR 19-JUL-1999; 99US-0144332.
 PR 19-JUL-1999; 99US-0144333.
 PR 19-JUL-1999; 99US-0144334.
 PR 19-JUL-1999; 99US-0144335.
 PR 20-JUL-1999; 99US-0144352.
 PR 20-JUL-1999; 99US-0144632.
 PR 20-JUL-1999; 99US-0144884.

PR 21-JUL-1999; 99US-0144814.
 PR 21-JUL-1999; 99US-0145086.
 PR 21-JUL-1999; 99US-0145087.
 PR 22-JUL-1999; 99US-0145085.
 PR 22-JUL-1999; 99US-0145087.
 PR 22-JUL-1999; 99US-0145089.
 PR 22-JUL-1999; 99US-0145192.
 PR 23-JUL-1999; 99US-0145145.
 PR 23-JUL-1999; 99US-0145218.
 PR 23-JUL-1999; 99US-0145224.
 PR 26-JUL-1999; 99US-0145276.
 PR 27-JUL-1999; 99US-0145913.
 PR 27-JUL-1999; 99US-0145918.
 PR 27-JUL-1999; 99US-0145919.
 PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146386.
 PR 02-AUG-1999; 99US-0146388.
 PR 02-AUG-1999; 99US-0146389.
 PR 03-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151067.
 PR 30-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.

Pred. No.: 1,23e-50 Length: 273
 Score: 561.00 Matches: 109
 Percent Similarity: 99.09% Conservative: 0
 Best Local Similarity: 99.09% Mismatches: 1
 Query Match: 54.47% Indels: 0
 DB: 21 Gaps: 0

US-10-020-338-8 (1-593) x AAF78883 (1-273)

QY 263 ATGGTCGCGGCAAGGTGACGTGAAGCGATAGAAACAGATAATCGCAGGTGAC 322
 1 MetGlyArgGlyLeuValGlnLeuLysArgIleGluAsnLysIleAsnArgGlnValThr 20
 Db 323 TTCTCCAAAGCCCGCAAGCGGCTCTTGAAGAGCGCGACAGATCTCCGCTCTGTGAC 382
 21 PheSerLysArgArgAsnGlyLeuLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40
 QY 383 GCGAGGTGCGCGTCATGCTCTTCCGCCAAAGCGACGCTATGAGTACGCCACCGAC 442
 41 AlaGluValAlaValIleValPheSerProLysGlyLysLeuLysGlnLysAlaThrAsp 60
 Db 443 TCCAGCATGACAAATTTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAGGCTCTT 502
 61 SerArgMetAspLysIleLeuGlnLysArgLysArgLysSerTyrAlaGlnLysAlaLeu 80
 QY 503 ATTGAGTGAATCTGAAAGTGAAGGAAATGGTCCAGCAATACAGAACTTAAAGCG 562
 81 IleSerAlaGlnSerGlnSerGlnLysArgLysArgLysSerTyrAlaGlnLysAlaLeu 100
 QY 563 AAGATTGAGACCAATACAAATATGTCACAG 592
 101 LysIleGlnThrIleGlnLysCysHisLys 110
 Db

RESULT 10

AAB73250
 ID AAB73250 standard; Protein; 267 AA.

AC AAB73250;

DT 14-MAY-2001 (first entry)

DE Rice MADS box protein.

KW Rice; MADS box; plant branching regulation; agriculture.

OS Oryza sativa.

XX MO200114559-A1.

PD 01-MAR-2001.

PF 18-AUG-2000; 2000WO-JP05537.

PR 19-AUG-1999; 99JP-0232318.

XX (TSUB) KUMIAI CHEM IND CO LTD.

PA (KOJI/) KOJIMA M.

PI Kojima M, Sasaki T, Nozue M, Shioiri H;

XX WPI; 2001-191647/19.

DR N-PSDB; AAF5749.

XX Rice MADS box gene for regulating plant branching to provide ornamental

PT or agricultural plants with value-added properties or increase in yield

PT Claim 2; Page 19; 43pp; Japanese.

XX The present sequence is the rice MADS box protein. The MADS box gene can

CC be used for regulating plant branching to provide ornamental or

CC agricultural plants. In addition, plants with value-added properties or

CC an increased yield can be produced using the MADS box gene.

XX SQ Sequence 267 AA;

Alignment Scores:

Pred. No.: 3.23e-50 Length: 267
 Score: 557.00 Matches: 108
 Percent Similarity: 98.18% Conservative: 0
 Best Local Similarity: 98.18% Mismatches: 2
 Query Match: 54.08% Indels: 0
 DB: 22 Gaps: 0

US-10-020-338-8 (1-593) x AAB73250 (1-267)

QY 263 ATGGTCGCGGCAAGGTGACGTGAAGCGATAGAAACAGATAATCGCAGGTGAC 322
 1 MetGlyArgGlyLysValGlnLeuLysArgIleGluAsnLysIleAsnArgGlnValThr 20
 Db 323 TTCTCCAAAGCCCGCAAGCGGCTCTTGAAGAGCGCGACAGATCTCCGCTCTGTGAC 382
 21 PheSerLysArgArgAsnGlyLeuLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40
 QY 383 GCGAGGTGCGCGTCATGCTCTTCCGCCAAAGCGACGCTATGAGTACGCCACCGAC 442
 41 AlaGluValAlaValIleValPheSerProLysGlyLysLeuLysGlnLysAlaThrAsp 60
 Db 443 TCCAGCATGACAAATTTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAGGCTCTT 502
 61 SerArgMetAspLysIleLeuGlnLysArgLysArgLysSerTyrAlaGlnLysAlaLeu 80
 QY 503 ATTGAGTGAATCTGAAAGTGAAGGAAATGGTCCAGCAATACAGAACTTAAAGCG 562
 81 IleSerAlaGlnSerGlnSerGlnLysArgLysArgLysSerTyrAlaGlnLysAlaLeu 100
 QY 563 AAGATTGAGACCAATACAAATATGTCACAG 592
 101 LysIleGlnThrIleGlnLysCysHisLys 110
 Db

RESULT 11

AAG33291
 ID AAG33291 standard; Protein; 142 AA.

AC AAG33291;

DT 18-OCT-2000 (first entry)

DE Zea mays protein fragment SEQ ID NO: 40314.

XX Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence; corn.

XX Zea mays subsp. mays.

XX EP103405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 29-MAR-1999; 99US-0126264.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0128845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 23-APR-1999; 99US-0130891.

Db 61 SerArgMetAspLysIleLeuGluArgTyrGluArgTyrSerTyrAlaGluLysAlaLeu 80
 QY 503 ATTTGCGTGAATCTGAAGTGGAGGAATGGTGCACGAATACAGAACTTAAGGCG 562
 Db 81 IIESeRAlaGluSerIuSerIuSerIuGluYasnTrpCysHsGluYrArgLysLeuYsAla 100
 QY 563 AAGATTGAGACCATACAAATAATGTCAAG 592
 Db 101 LysIleGluThrIleGlnLysCysHsLys 110

RESULT 8
 AA67553

ID AA67553 standard; Protein; 273 AA.

XX AA67553;

DT 19-MAY-2000 (first entry)

XX Zea mays ZAPI protein.

Seed plant; floral meristem; mutation; TFL gene; CAL; reproduction; plant breeding; API protein.

XX Zea mays.

OS US6025543-A.

PN 15-FEB-2000.

XX 05-JUN-1996; 96US-0655241.

XX 05-JUN-1996; 96US-0655241.

XX (REGC) UNIV CALIFORNIA.

XX Yanofsky MF;

DR WPI: 2000-181843/16.

DR N-PSDB; AA257057.

PT New transgenic seed plant exhibiting early reproductive development

PT comprises a CAULIFLOWER encoding nucleic acid and a non-mutant

PT endogenous TERMINAL FLOWER gene -

PS Claim 15; Columns 59-64; 51pp; English.

XX The invention relates to a new non-naturally occurring seed plant that
 CC comprises a first ectopically expressible nucleic acid molecule encoding
 CC a floral meristem identity gene product, provided that the seed plant
 CC does not contain a mutation in an endogenous TERMINAL FLOWER (TFL) gene.
 CC that results in ectopic expression of CAL. The non-naturally occurring
 CC seed plant exhibits early reproductive development. The method of
 CC promoting early reproductive development can make breeding of long
 CC generation seed plants such as trees practical. The method can be used to
 CC increase floral meristem identity gene product expression in different
 CC crop fields at different times, resulting in a staggered time of harvest
 CC for the different fields. The present sequence represents a Zea mays
 CC API protein.

XX Sequence 273 AA;

XX Alignment Scores:

Pred. No.: 1.23e-50 Length: 273
 Score: 561.00 Matches: 109
 Percent Similarity: 99.09% Conservative: 0
 Best Local Similarity: 99.09% Mismatches: 1
 Query Match: 54.47% Indels: 0
 DB: 21 Gaps: 0

US-10-020-338-8 (1-593) x AA67553 (1-273)

QY 263 ATGGTCGGCGAAGGTGAGTGAAGCGAGTAGAGACAGATTAATCGCGAGTGACC 322

Db 1 MetGlyArgGlyLysValGlnLeuLysArgIleGluAsnLysIleAsnArgGlnValThr 20
 QY 323 TTCTCCAAAGCGCGGACGAGGCTCTGAAGAAAGCGCAGAGATCTCCGCTCTGTGAC 382
 Db 21 PheSerLysArgArgAsnGlyLeuLeuLysValAlaHsGluIleSerValLeuGlyAsp 40
 QY 383 GCGAGGTGCGCCGTCATGCTCTTCCGCCAAAGCAAGCTTATAGTACGCCACGAC 442
 Db 41 AlaGluValAlaValIleValPheSerProLysGlyLysLeuTyrGluTyrAlaThrAsp 60
 QY 443 TCCAGCATGAGACAAATTTCTTAACGTATAGCGCTACTCTTATGCTGAAAAGCTCTT 502
 Db 61 SerArgMetAspLysIleLeuGluArgTyrGluArgTyrSerTyrAlaGluLysAlaLeu 80
 QY 503 ATTTGCGTGAATCTGAAGTGGAGGAATGGTGCACGAATACAGAACTTAAGGCG 562
 Db 81 IIESeRAlaGluSerIuSerIuSerIuGluYasnTrpCysHsGluYrArgLysLeuYsAla 100
 QY 563 AAGATTGAGACCATACAAATAATGTCAAG 592
 Db 101 LysIleGluThrIleGlnLysCysHsLys 110

RESULT 9

AA78883

ID AA78883 standard; Protein; 273 AA.

XX AA78883;

DT 19-MAY-2000 (first entry)

XX Corn APETALA1 (API) amino acid sequence.

APETALA1; API; floral meristem identity; early reproductive development;
 KW transgenic plant; selective breeding programme; disease resistance; corn.

OS Zea mays.

OS US6025483-A.

PN 15-FEB-2000.

XX 05-JUN-1996; 96US-0655227.

XX 05-JUN-1996; 96US-0655227.

XX (REGC) UNIV CALIFORNIA.

XX Yanofsky MF;

DR WPI: 2000-181839/16.

DR N-PSDB; AA92144.

PT Purified nucleic acids encoding APETALA 1 (API) proteins, promote early

PT reproductive development in seed plants, useful for accelerating

PT selective breeding programmes -

PS Claim 1; Column 63-64; 50pp; English.

XX This sequence represents the APETALA1 (API) amino acid sequence from
 CC corn. API is a floral meristem identity product, that promotes conversion
 CC of shoot meristem to floral meristem in an angiosperm. Vectors containing
 CC the API gene can be used to create transgenic plants. API nucleotide
 CC sequences can be used to promote early reproductive development in seed
 CC plants which is useful for accelerating selective breeding programmes
 CC that require several rounds of crossing to produce plants with disease
 CC and insect resistance. The nucleotide sequences are particularly useful
 CC for promoting early reproductive development in long generation seed
 CC plants such as trees.

XX Sequence 273 AA;

XX Alignment Scores:

OS Zea mays.
XX WO9746078-A1.
XX 11-DEC-1997.
PD
XX 05-JUN-1996; 96WO-US09453.
XX 05-JUN-1996; 96WO-US09453.
XX (REGC) UNIV CALIFORNIA.
XX Yanofsky MF;
PI WPI; 1998-041770/04.
DR N-PSDB; AAV02763.
XX
XX Nucleic acids encoding AP1 floral meristem identity gene product
PT from cauliflower and maize - useful for promoting early reproductive
development and controlling the time of seed-derived crop harvest in
e.g. grapes, beans, corn, wheat, etc
XX
XX Claim 1; Page 127-128; 156pp; English.
PS
XX This protein comprises maize floral meristem identity gene product
CC ZAP1, the orthologue of the Arabidopsis APETALA (AP1) gene product
CC (see AAW39131) that is involved in the conversion of shoot meristem
CC to floral meristem. Mutation of the AP1 gene results in replacement
CC of basal flowers by inflorescence shoots that are not subtended by
CC flowers. The invention relates to an expression vector comprising
CC a nucleic acid sequence encoding a floral meristem gene product
CC operably linked to a heterologous regulatory element (see
CC AAV02770-75). The floral meristem gene product is selected from AP1,
CC LFY (LEAFY) and CAL (CAULIFLOWER) (see AAW39131-38). The expression
CC vector is used to convert shoot meristem tissue to floral meristem
CC tissue in transgenic plants, especially angiosperms or gymnosperms,
CC thereby promoting early reproductive development in these plants.
CC This can be used to manipulate the time of crop harvest and to
CC hasten breeding time.
XX
XX
SQ Sequence 273 AA;
Alignment Scores:
Pred. No.: 1,236-50 Length: 273
Score: 561.00 Matches: 109
Percent Similarity: 99.09% Conservative: 0
Best Local Similarity: 99.09% Mismatches: 1
Query Match: 54.47% Indels: 0
Gaps: 0
US-10-020-338-8 (1-593) x AAW39134 (1-273)
QY 263 ATGGGTTCGGCGGAGGTGAGCTGAGCGATAGAGCAAGATAATCGGAGGTGACC 322
DB 1 MetGlyArgGlyLysValGlnLeuLysArgGlnLeuLysValGlnLeuLysValGlnLeu 20
QY 323 TTCTCCAGCGCGGCAACGGGCTCTGGAAGAGCGGCAAGATCTCCGCTCTGTGAC 382
DB 21 PheserLysArgArgLysGlnLeuLysValGlnLeuLysValGlnLeuLysValGlnLeu 40
QY 383 GCGGAGGTGCGGCGTATCTGCTTCTCCCGAAGGCAAGCTTATAGTACGCAACGAC 442
DB 41 AlaGlnValAlaValAlaValAlaPheSerProLysGlnLeuLysValGlnLeuLysValGlnLeu 60
QY 443 TCCAGATGAGCAAAATTTCTTGAACGTTATGACGCTACTCTATGCTGAAAAGGCTCTT 502
DB 61 SerArgMetArgLysLysLeuGlnArgLysGlnArgLysLysValGlnLeuLysValGlnLeu 80
QY 503 ATTTCAGCTGAATCTGAAAGTGAAGGAAATTTGGTCCACGATACAGAAATCTTAAAGCG 562
DB 81 IleSerAlaGlnSerGlnSerGlnGlnLysAsnTrpCysHisGlnLysValGlnLeuLysValGlnLeu 100
QY 563 AAGATTGAGACATACAAATAATGTCACAG 592

DB 101 LysIleGlnThrIleGlnLysCysHisLys 110
RESULT 7
AAB19244
ID AAB19244 standard; Protein; 273 AA.
XX
XX AAB19244;
AC
XX
XX 19-FEB-2001 (first entry)
DT
XX
XX
DE Amino acid sequence of a APETALA1 (AP1) polypeptide.
XX
XX APETALA1; AP1; floral meristem identity gene; CAULIFLOWER; CAL; LEAFY;
XX LFY; floral meristem; early flowering.
OS
XX Zea mays.
XX
XX US6127123-A.
XX
XX 03-OCT-2000.
PD
XX
XX 09-SEP-1998; 98US-0149976.
XX
XX 26-JAN-1996; 96US-0592214.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Yanofsky MF;
PI WPI; 2000-618379/59.
DR N-PSDB; AAC61410.
XX
XX Identifying a Brassica having a cauliflower phenotype involves
PT detecting a polymorphism associated with cauliflower locus comprising a
PT modified cauliflower allele that does not encode active cauliflower
PT gene product
XX
XX Example 1; Fig 4A-B; 93pp; English.
XX
XX The present sequence represents an APETALA1 (AP1) polypeptide. The AP1
CC polypeptide is an ecologically expressible floral meristem identity
CC gene product. The specification also describes CAULIFLOWER (CAL) and
CC LEAFY (LFY) gene products. CAL is involved in the conversion of shoot
CC meristem to floral meristem. CAL is highly conserved among different
CC angiosperms. The CAL polynucleotides may be used to shoot meristem to
CC floral meristem, and to promote early flowering in angiosperms.
XX
XX
SQ Sequence 273 AA;
Alignment Scores:
Pred. No.: 1,236-50 Length: 273
Score: 561.00 Matches: 109
Percent Similarity: 99.09% Conservative: 0
Best Local Similarity: 99.09% Mismatches: 1
Query Match: 54.47% Indels: 0
Gaps: 0
US-10-020-338-8 (1-593) x AAB19244 (1-273)
QY 263 ATGGGTTCGGCGGAGGTGAGCTGAGCGATAGAGCAAGATAATCGGAGGTGACC 322
DB 1 MetGlyArgGlyLysValGlnLeuLysArgGlnLeuLysValGlnLeuLysValGlnLeu 20
QY 323 TTCTCCAGCGCGGCAACGGGCTCTGGAAGAGCGGCAAGATCTCCGCTCTGTGAC 382
DB 21 PheserLysArgArgLysGlnLeuLysValGlnLeuLysValGlnLeuLysValGlnLeu 40
QY 383 GCGGAGGTGCGGCGTATCTGCTTCTCCCGAAGGCAAGCTTATAGTACGCAACGAC 442
DB 41 AlaGlnValAlaValAlaValAlaPheSerProLysGlnLeuLysValGlnLeuLysValGlnLeu 60
QY 443 TCCAGATGAGCAAAATTTCTTGAACGTTATGACGCTACTCTTATGCTGAAAAGGCTCTT 502

XX 25-FEB-2000; 2000EP-0301439.
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 PR 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128234.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES						
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1	570	55.3	164	21	AAG33290	Zea mays protein f
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3	561	54.5	273	19	AAW69328	Zea mays API prote
4	561	54.5	273	19	AAW43112	APETALAI gene prod
5	561	54.5	273	19	AAW43329	Arabidopsis floral
6	561	54.5	273	19	AAW39134	Maize floral meris
7	561	54.5	273	21	AAAB19244	Amino acid sequenc
8	561	54.5	273	21	AAAY67553	Zea mays ZAP1 prot
9	561	54.5	273	21	AAAY78883	Corn APETALAI (AP1
10	557	54.1	267	22	AAAB73250	Rice MADS box prot
11	554	53.8	142	21	AAG33291	Zea mays protein f
12	554	53.8	270	22	AAAB68357	Amino acid sequenc
13	435.5	42.3	307	21	AAAG31120	Zea mays protein f
14	428	41.6	253	18	AAAG23812	Brassica oleracea
15	428	41.6	253	19	AAW69329	Brassica oleracea
16	428	41.6	253	19	AAW43110	APETALAI gene prod
17	428	41.6	253	19	AAW43132	Brassica floral me
18	428	41.6	253	19	AAW43327	Brassica floral me
19	428	41.6	253	19	AAAB19242	Amino acid sequenc
20	428	41.6	253	21	AAAY67551	B. oleracea API pr
21	428	41.6	253	21	AAAY78881	Brassica oleracea
22	424	41.2	255	18	AAW23811	Arabidopsis floral
23	424	41.2	255	20	AAW67571	Arabidopsis LEAFY
24	424	41.2	256	19	AAW43109	APETALAI gene prod
25	424	41.2	256	19	AAW39131	Arabidopsis floral
26	424	41.2	256	19	AAW43326	Arabidopsis floral
27	424	41.2	256	21	AAAG17300	Arabidopsis thalia
28	424	41.2	256	21	AAAG52893	Arabidopsis thalia
29	424	41.2	256	21	AAAY84912	Amino acid sequenc
30	424	41.2	256	21	AAAY78880	A. thaliana API pr
31	424	41.2	300	21	AAAB19241	APETALAI (AP1) nuc
32	424	41.2	302	19	AAW69327	Amino acid sequenc
33	424	41.2	302	19	AAW23813	Arabidopsis thalia
34	422	41.0	255	18	AAW69330	Cauliflower floral
35	422	41.0	255	19	AAW69331	Brassica oleracea
36	422	41.0	255	19	AAW43111	APETALAI gene prod
37	422	41.0	255	19	AAW43328	Cauliflower floral
38	422	41.0	255	19	AAW39133	Cauliflower floral
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40	422	41.0	255	21	AAAY67552	B. oleracea var. b
41	422	41.0	255	21	AAAY78882	Cauliflower APETAL
42	420	40.8	246	20	AAW69318	Petunia MADS box t
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